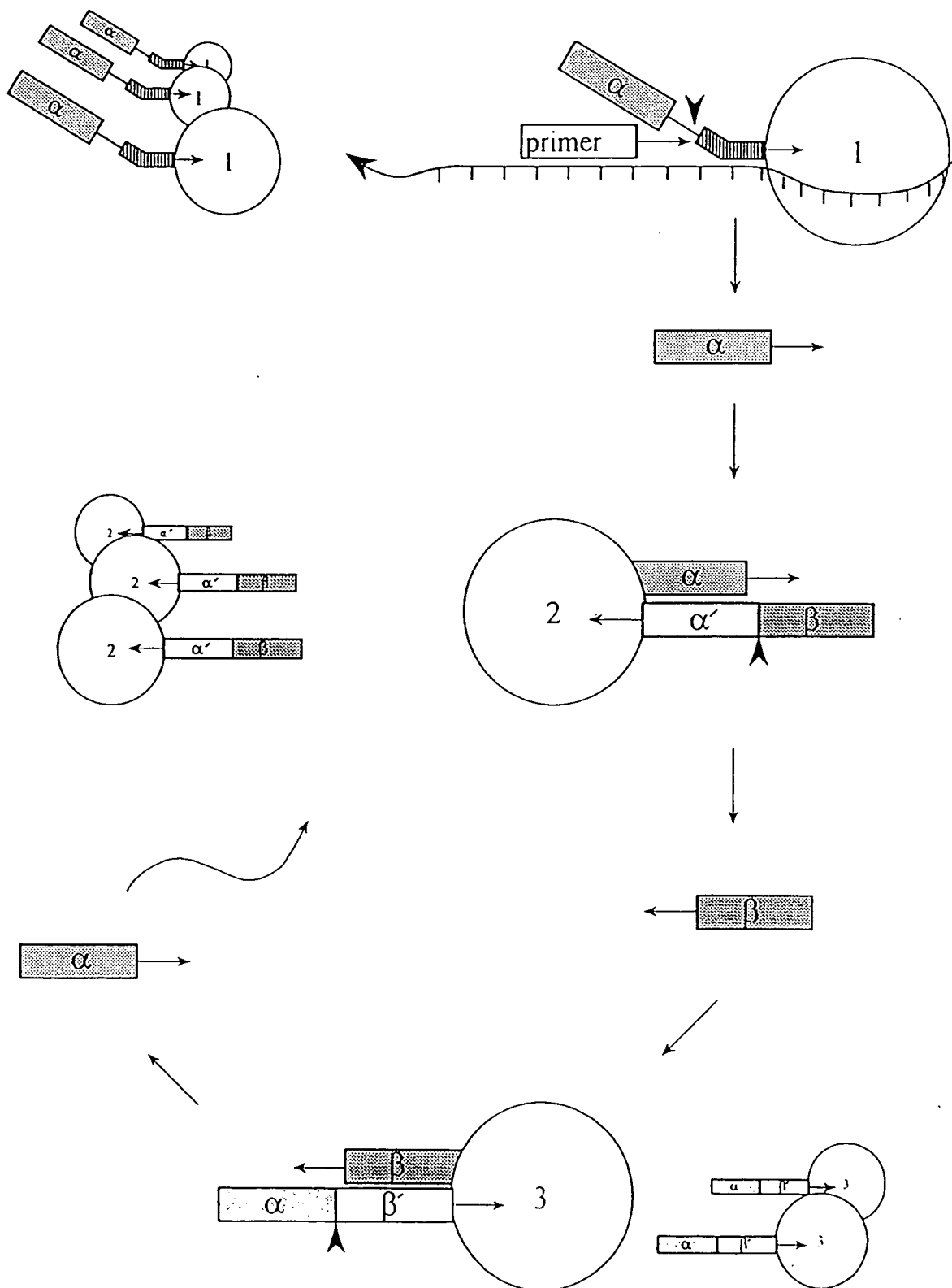


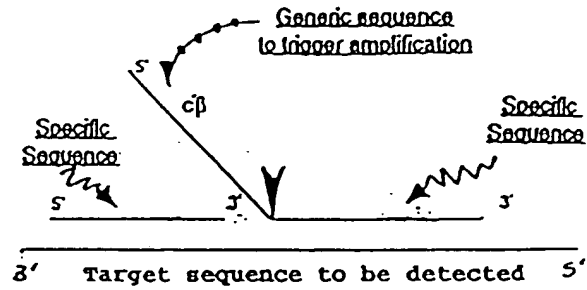
FIGURE 1A



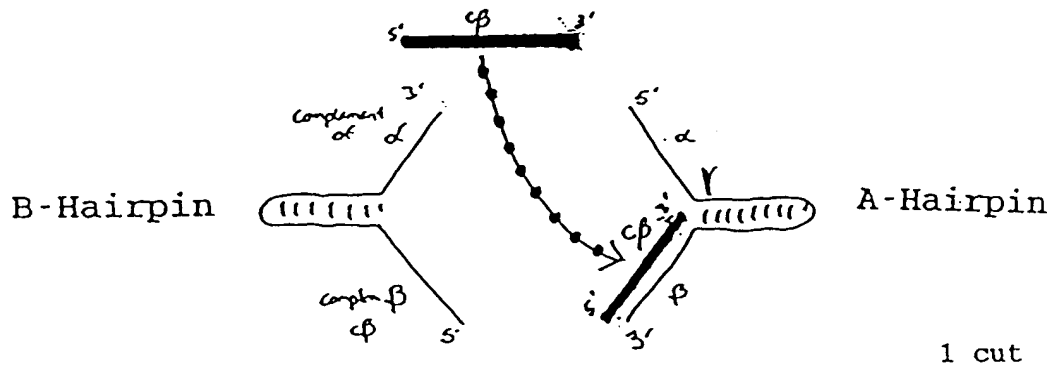
10074328, 021202

FIGURE 1B

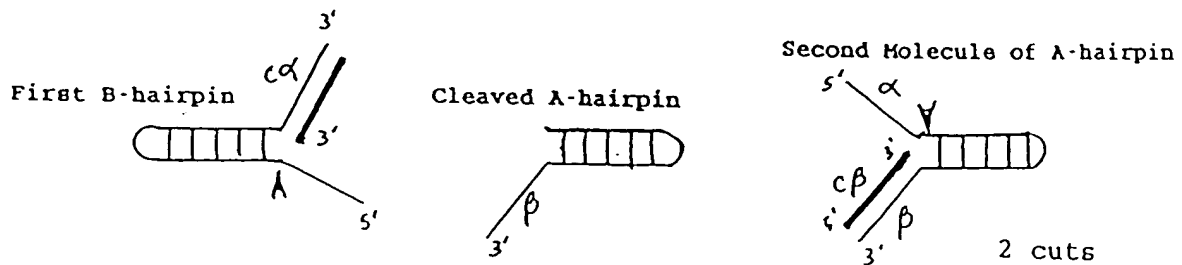
PART ONE: TRIGGER REACTION



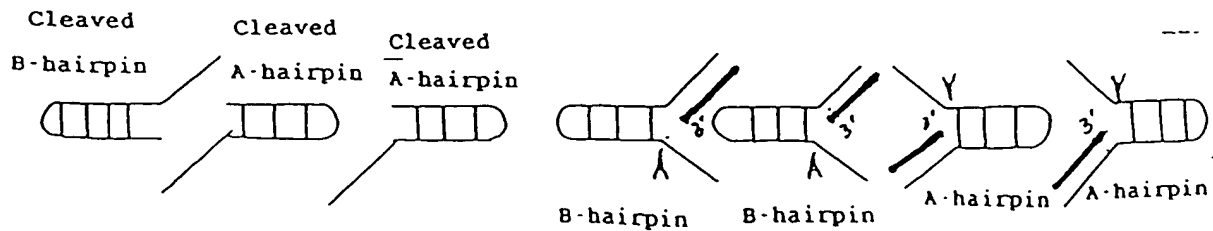
PART TWO: DETECTION REACTION



Denature, anneal



Denature, anneal



2

20220103 021202 10074323

FIGURE 2

MAJORITY (SEQ ID NO:7)	ATGXGGCGATGCTTCCCTCTTTGAGCCCAAAGCGCGGCTCCTCCTGGTGGACGGCCACACCTGGCCCT	
DNAPTAD (SEQ ID NO:1)	... AG... G... .. G... ..	70
DNAPTFL (SEQ ID NO:2)	... .. G... ..	67
DNAPTTH (SEQ ID NO:3)	... GA... .. A... ..	70
MAJORITY	ACCCACCTTCTTCGCCCTGAAGGCCCTCACCCACAGCCCGGGCGGAACCGGTCCAGCGGCTCTACGGCTT	
DNAPTAD	... .. GA... ..	140
DNAPTFL	... .. T... .. G... ..	137
DNAPTTH	... .. G... ..	140
MAJORITY	CCCCAAGAGCCCTCCTCAAGGCCCTGAAGGAGGAGCGGGGACXXGGCGGCTGXTGGTCTCTTGACGGCCAAG	
DNAPTAD	... .. C... ..	207
DNAPTFL	... .. A... .. GT... T... ..	204
DNAPTTH	... .. T... .. AA... C... CT... ..	210
MAJORITY	GGCCCGCTCCTTCGCCCCACGAGGCCTACGAGGCCTACAAAGCGGGCGGGCGGGCCCGGAGGACCTTC	
DNAPTAD	... .. G... ..	277
DNAPTFL	... .. GA... ..	274
DNAPTTH	... .. C... ..	280
MAJORITY	CCCCGGCAGCTCGCCCTCATCAAGGAGGCTGCTGGACCTCCTGGCGGCTTGGCGGCGCTCGAGGTCGCCCGGCTA	
DNAPTAD	... .. A... ..	347
DNAPTFL	... .. G... .. T... .. A... C... .. T... .. G... ..	344
DNAPTTH	... .. T... .. T... .. A... C... ..	350

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CGAGCGGACGACGTXCTGGCCACCGCTGGCCAAAGAGCGGGAAGAGGGGTACGAGGTCGCCCATCCTC	
DNAPTAA (SEQ ID NO:1)	.....G.....G.....C.....C.....	417
DNAPTFL (SEQ ID NO:2)	T.....G.....GG.....	414
DNAPTTH (SEQ ID NO:3)	.....T..C.....	420
MAJORITY	ACCGCGGACCGGACGCTCTACGAGGTCCTTCGGAGCGGATCGCCGTCCTCCACCCGAGGGGTACCTCA	
DNAPTAA (SEQ ID NO:1)	.....AAA.....T.....CA.....	487
DNAPTFL (SEQ ID NO:2)	..T.....G..G.....A.....T.....G..	484
DNAPTTH (SEQ ID NO:3)	.....A..G.C.....G.....CC.....	490
MAJORITY	TCACCGCGGCGTGGCTTTGGGAGAAAGTACGGCGCTGAGCGCGGAGCAGTGGGTGGACTACCGGGCCCTGGC	
DNAPTAA (SEQ ID NO:1)	.....C.....A.....A.....C..C.....CC.....A..	557
DNAPTFL (SEQ ID NO:2)	.....AC.....C.C.....	554
DNAPTTH (SEQ ID NO:3)	.....A.....C.....T..C.....C..T	560
MAJORITY	CGCGGACCCCTCCGACAAACCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXCAAGCTCCTCXAG	
DNAPTAA (SEQ ID NO:1)	C.....GAG.....T'.....G..GAG.....T..GG..	627
DNAPTFL (SEQ ID NO:2)	.....G..T..A.....G.....A..G.....A..CGC	624
DNAPTTH (SEQ ID NO:3)	.....TC.....A..	630
MAJORITY	CAGTGGCGGACCGCTGGAAAAACCTCCTCAAGAAACCTGGACCGGGGTGAAGCCCGCC...CXTCCGGGAGAGA	
DNAPTAA (SEQ ID NO:1)	.....GC.....C.....A.....	694
DNAPTFL (SEQ ID NO:2)	.....T..C..C.....A.....T.....T..G.....C	691
DNAPTTH (SEQ ID NO:3)	.....A.....A.....A.AAAA.G.....	700

f



FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CGGGGXTCTCCTCGCCCAAGGACCTGGCCGCTTTTGGCCCTGAGGGAGGGGCTXGACCTCTGCCCCGGGACG	
DNAPTAD	(SEQ ID NO:1)	.....G..T.....A.....AG.....C.....A.....T.G.....CC.....G.....	1111
DNAPTFL	(SEQ ID NO:2)	.....AA.....G.....G.....C.....G.....T.C..A..A.....	1120
DNAPTTH	(SEQ ID NO:3)	.....C.....C.....C.....TC.....G..A.....G.....	
MAJORITY		ACCCCATGCTCCTCGCCCTACCTCCTCGAGCCCTTCCAAACACACCCCGGAGGGGCTGGCCCGCGCTACGG	
DNAPTAD		.....T.....	1184
DNAPTFL		.....G.....T.....T.....T.....	1181
DNAPTTH		.....G.....G.....	1190
MAJORITY		CGGGGACTGGACGGAGGAXGGGGGGGAGGGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXGGAG	
DNAPTAD		G.....G.....G.....GC.....T.....G.....GCC.....GTG...G..	1254
DNAPTFL		.....T.....A.....GG.....C.G.....A..C...AAA....	1251
DNAPTTH		.....C..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY		CGCCCTCAGGGGGAGGAGGCTCCTTGGCTTTACGAGGAGGTGGAGAACCCCTTCCCGGCTCCTCG	
DNAPTAD		A.G.....A..A..A..AC.C..G.....G.....G.....GCT.....	1324
DNAPTFL		.....A.....A..A..AC.C..G.....G.....G.....GT...	1321
DNAPTTH		.....C.....A.....A.....C.....A.....C.....	1330
MAJORITY		CCACATCGAGGCCACGGGGGTXCGGGCTGGACCTGGCCCTACCTCCAGGGCCCTXTGCCCTGGAGGTGGCGGA	
DNAPTAD		.....G..C.....G..C.....T...AG...T.G.....C...	1394
DNAPTFL		.....G.....C.....C.....T.....C.....A..C	1391
DNAPTTH		.....G.....A.....A.....T.....T.....C.T.....	1400

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCCGGCCGCTCGAGGAGGAGGTCTTCGGGCTGGCGGGCCACCCCTTCAACCTCAACTCCCGGGAC	1464
DNAPTAA (SEQ ID NO:1)	.....GC.....CC.....	1461
DNAPTTL (SEQ ID NO:2)	...G.G...AG..G.....	1472
DNAPTH (SEQ ID NO:3)	.....T...G.....	
MAJORITY	CAGCTGGAAGGGTGCCTCTTTACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGGAGACXGGCAAGC	
DNAPTAA	.....G.....A.....	1534
DNAPTTL	.....GC.....G.C..G..T.....	1531
DNAPTH	.....TA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCACGAGCGCGCGTGGTGGAGGCGCTXCGXGAGGCGCCACCCCATCGTGGAGAAGATCCTGCAGTA	
DNAPTAA	.....C.....C..C.....	1604
DNAPTTL	.....T.....G..A.....CGGC.....	1601
DNAPTH	.....G.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCGCTGCCXGXCCTCGTCCACCCGAGGACGGGGC	
DNAPTAA	.....G...G.....T.....G.A...A.....	17
DNAPTTL	.....A.....C.C...G.....A...C...	16
DNAPTH	.....C.G.....C..AAG.....G.....	16
MAJORITY	CGCCCTCCACACCCGCTTCAACCAGACGGCGCCACGGGCGAGGCTTAGCTCCGACCCCAACCTGC	
DNAPTAA	.....A.....T.....C..	1744
DNAPTTL	.....C.....TCC.....	1741
DNAPTH	.....G.....G.....	1750

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	AGAACATCCCCGTCCGCCACCCXCTGGCCACAGGATCCGCCCGGCCCTTCGTGCCCGACGACGCGTCCGT	
DNAPTAA	(SEQ ID NO:1)	.....G..T..G.....A..C.....G...C..	1814
DNAPTTL	(SEQ ID NO:2)	.....G.....T.....C.C.....A.....C.....C.....	1811
DNAPTTH	(SEQ ID NO:3)	.....CT.....C.....C.....T.....C.....T.....C.....	182
MAJORITY		CTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCGTGCCCCACCTCTCCGGCGACGAGAACCTG	
DNAPTAA		A.....T.....T.....A.....G.....C.....	1884
DNAPTTL		.C.....T.....C.....T.....T.....C.....	1881
DNAPTTH		.....C.....C.....C.....A.....A.....	1890
MAJORITY		ATCCGGGTCTTCAGAGGGAGGGACATCCACACCCACAGCCGACGCTGCATGTTCCGGCGTCCCCCGCG	
DNAPTAA		.....C.....C.....GG.....G.....G.....	1954
DNAPTTL		.....T.....T.....T.....T.....T.....	1951
DNAPTTH		A.....A.....A.....A.....A.....	1960
MAJORITY		AGGCCGTGCACCCCTGATCCGCCCGCGCGCCCAAGACCATCAACTTCGGGGTCCCTCTACGGCGATGTCGGC	
DNAPTAA		.....A..G..A.....T.....G.....G.....G.....	2014
DNAPTTL		.....A.....T.....GG.G.....C.....C.....	2021
DNAPTTH		.....A.....T.....GG.G.....C.....C.....	2030
MAJORITY		CCACCGGCTCTCCGAGGAGGCTGCCATCCCCTACGAGGAGCGCGTGGCCCTTCATTGACCGCTACTTCCAG	
DNAPTAA		.....A.....A.....T.....CCA.....T.....T.....	2094
DNAPTTL		.....GG.....T.....T.....T.....T.....	2091
DNAPTTH		...TA.G.....T.....T.....A.....A.....	2100



FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCCCAAAGCTGGGGGCTGGATTGAGAAAGACCCCTGGAGGAGGGCAGGAGCGGGGGTACGTCGAGA	2164
DNAPTAD (SEQ ID NO:1)	.....	2161
DNAPTFL (SEQ ID NO:2)	A.....GG.....C.....C.CC.....T.....	217
DNAPTTH (SEQ ID NO:3)	.....A.....A.....G.....A.....C.....A.....	
MAJORITY	CCCTCTTCGGCGCGCGGGCTACGTGCCCGACCTCAACGGCCGGGTGAAGAGCGTCCGGGAGCGCGCGCGA	
DNAPTAD	.....C.....A.....AG.G.....C.....	2234
DNAPTFL	.....T.....C.....	2231
DNAPTTH	.....AA.AA.....CA.....C.....	2240
MAJORITY	GGGCATGGCCCTTCAACATGCCCGTCCAGGGCAGCCCGCCGACCTCATGAAGCTGGCCCATGCTGAAGCTC	
DNAPTAD	.....T.....	2304
DNAPTFL	.....G.....CG.....T.....	2301
DNAPTTH	.....C.....	2310
MAJORITY	TTCCCGCGGCTXCAGGAAATGGGGGCGCAGGATGCTCCTXCAGGTCCAGCAGGAGCTGCTCCTCGAGCGCCC	
DNAPTAD	A.....GG.....T.....	2371
DNAPTFL	.....T.....C.....TT.G.....G.....	2380
DNAPTTH	.....C.C.G.....C.C.....C.....C.....	
MAJORITY	CCAAAGAGCGCGCGGAGCGGTGGCCCGCTTGGCCCAAGGAGGTCAATGGAGGGGGCTCTATCCCCCTGGCCGT	
DNAPTAD	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	.....G.C.....AG.....A.....GG.....CAG.....	2441
DNAPTTH	.....C.C.....C.....A.....G.....C.....AA..C.....C.....	2450

202F20" 82E4.00T

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CCCCCTGGAGGCTGGAGGCTGGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG	
DNAPTAD	(SEQ ID NO:1)	.....A.....	GA
DNAPTR	(SEQ ID NO:2)	.....GC.....	.....
DNAPTH	(SEQ ID NO:3)	.....T.....	GT...

2499  
2496  
2505

202120" B2E400T

FIGURE 3

MAJORITY (SEQ ID NO:8) MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRCEPVQAVYGFAKSLKALKEDG· DAVXVVFDAK

TAQ PRO (SEQ ID NO:4) · RG····· H····· I·····  
TRL PRO (SEQ ID NO:5) ······ V·V·····  
TTH PRO (SEQ ID NO:6) · E····· YK·F····· 70

MAJORITY APSFRHEAYEAYKAGRAPTEDFPROLALIKELVDLLGLXRLEVPCGYEADDVLATLAKKAEKEGYEVRI L

TAQ PRO ······ GC····· A····· S····· 139  
TRL PRO ······ V····· F····· R····· 138  
TTH PRO ······ FT····· ······ ······ 140

MAJORITY TADRDLYQLLSDRIAVLHPGYLITPAWLWEKYGLRPEOWVDYRALXGDPSONLPGVKIGI CEKTAXKLLX

TAQ PRO ······ K····· H····· ······ D·A····· T·E····· R····· E 209  
TRL PRO ······ E····· I····· ······ Y····· A····· I····· OR·IR 208  
TTH PRO ······ V····· V····· H····· E····· F····· V····· L····· K 210

MAJORITY EWGSLLENLLKNLDRVKP· XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPOREGLRAFLERLF

TAQ PRO ······ A····· L····· AL····· L····· D··K··WD·AK····· K····· R·····  
TRL PRO ······ FQH·O····· SL····· LO·G·A·A·RK·O·H····· GR·T·NL·····  
TTH PRO ······ ENV····· K·L··R·LE··R····· L·OG····· 277  
280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMYAEALLA AARXGRVHRAXDPLXGLRDLKEV

TAQ PRO ······ S····· ······ ······ K····· D····· G····· PE·YKA····· A 348  
TRL PRO ······ G····· A····· ······ L·SF····· ······ G·WE·L··O··R····· G· 347  
TTH PRO ······ A·AP····· ······ ······ K····· C·D····· A··A··K····· 350

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FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKDLAVLALREGLDLXPCDDPMLLAYLLDPSNTTPEGVARRYGGEWTEOGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)	.....S.....G.P.....	.....E.....A.....A...WG
TRL PRO (SEQ ID NO:5)	.....I.....F.E.....	.....A.....QT.KE
TTH PRO (SEQ ID NO:6)	.....S.....V.....	.....AH.....HR..LK 420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLOVAYLOALSLEVAEEIARRLEEEVFRLAGHPFNLNSRD	
TAQ PRO	.....R...R...A.....R.....	.....A.....A.....488
TRL PRO	.....K.....E.....R.....	.....EA.V.Q.....487
TTH PRO	.....K.....H.....	.....L.....490
MAJORITY	QLERVLFDGLPLAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTKLKNTYIDPLXLVHPRTG	
TAQ PRO	.....	.....S.....D.I.....558
TRL PRO	.....	.....DR.....A...K...557
TTH PRO	.....R...L...Q.....	.....H.....V...S...560
MAJORITY	RLHTRFNQTATATGRLSSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSGDEHL	
TAQ PRO	.....	.....L.....627
TRL PRO	.....	.....V...V.....627
TTH PRO	.....	.....A..A.....630
MAJORITY	IRVFQEGRDIHTQTASWMFGUPPEAVDPLMRRAAKTINFGVLYGMSAHL SOELAI PYEEAVAFIER YFO	
TAQ PRO	.....E.....R.....	.....Q.....698
TRL PRO	.....S...G.....	.....G...S.....697
TTH PRO	.....K.....	.....V.....700

202120" B2E4200T

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRAWI EKTLEEGRRRGYVETLFCRRRYVPDLNARVKSUREAAERMAFNMPVOGTAADLMKLA MVKL	
TAQ PR0 (SEQ ID NO:4)	.....E.....	70
TRL PR0 (SEQ ID NO:5)	Y.....G.....	767
TTT PR0 (SEQ ID NO:6)	.....K.....	770
MAJORITY	F PRLXEMGARM LLOVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PR0	.....E.....	833
TRL PR0	.....Q.L.....	831
TTT PR0	.....R.....L.....QA.....E.....A..KA.....M.....G	835

# FIGURE 4

Genes for Wild-Type and Pol(-) DNAPTaq

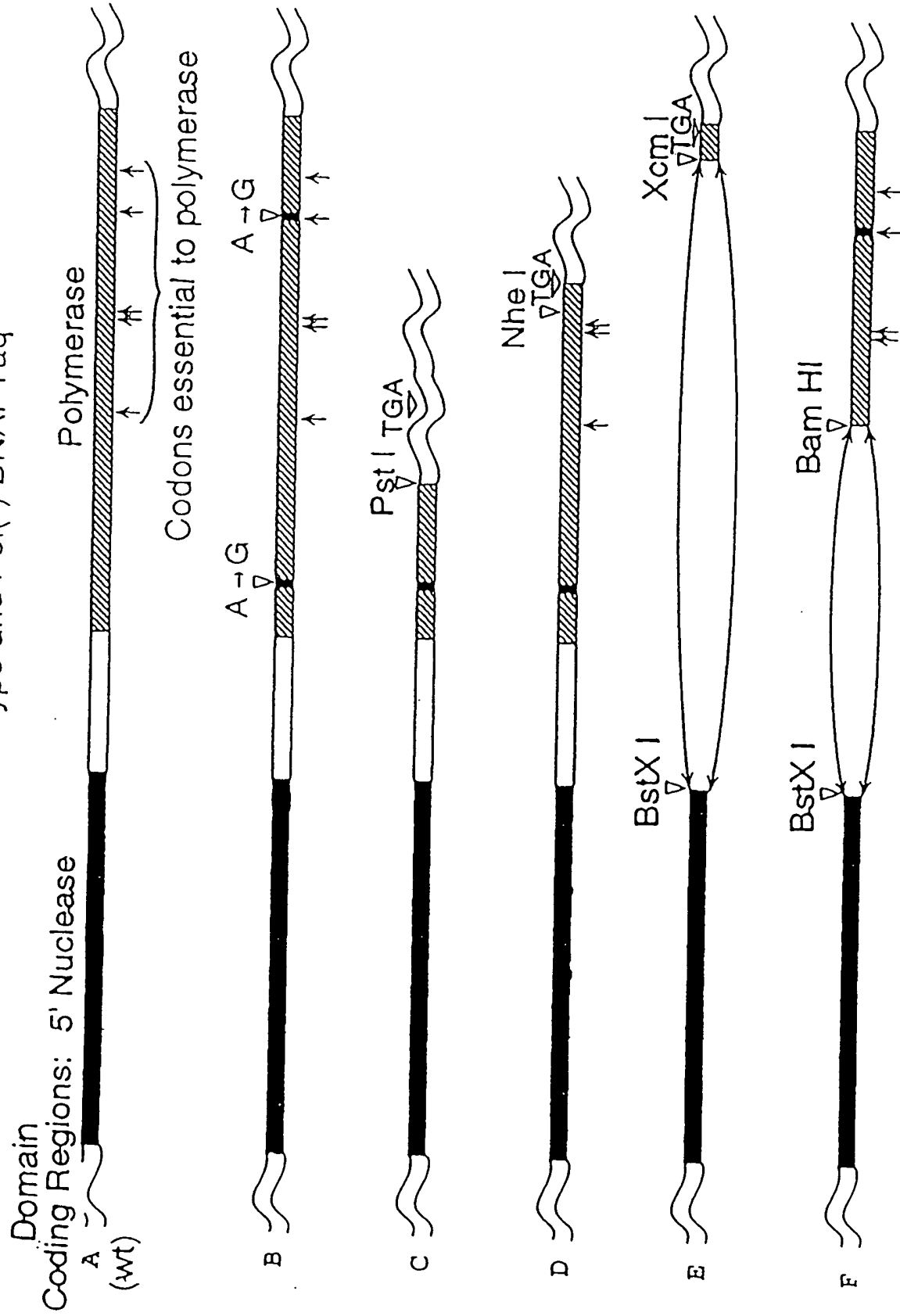


FIGURE 5

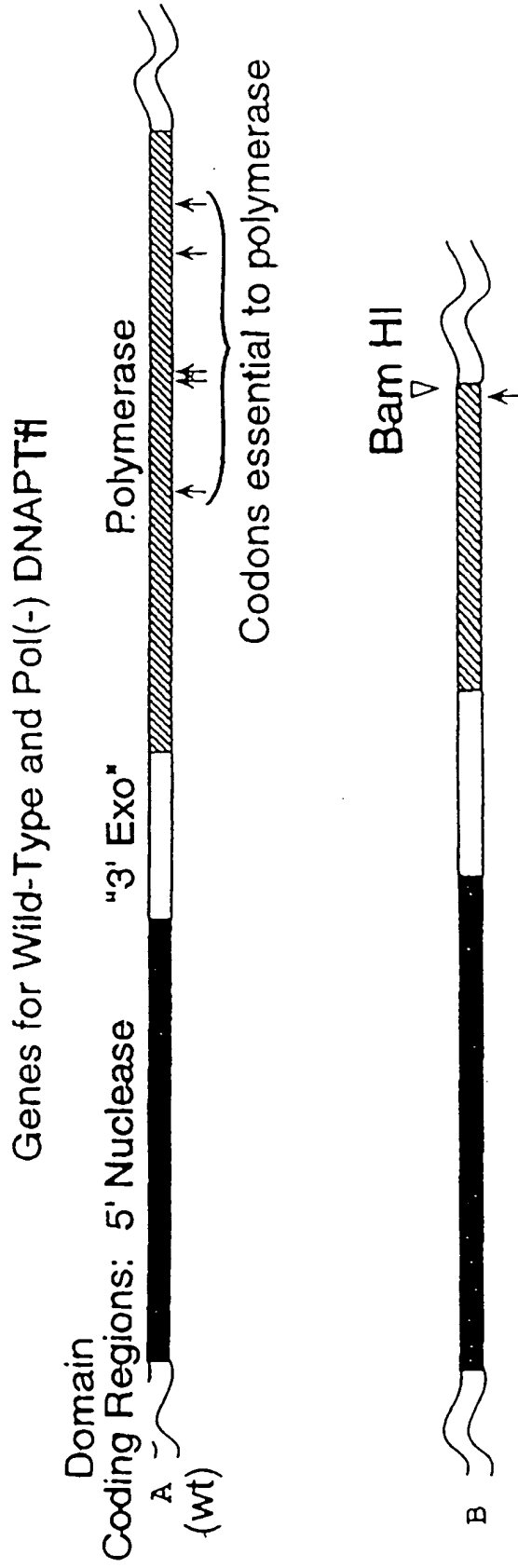
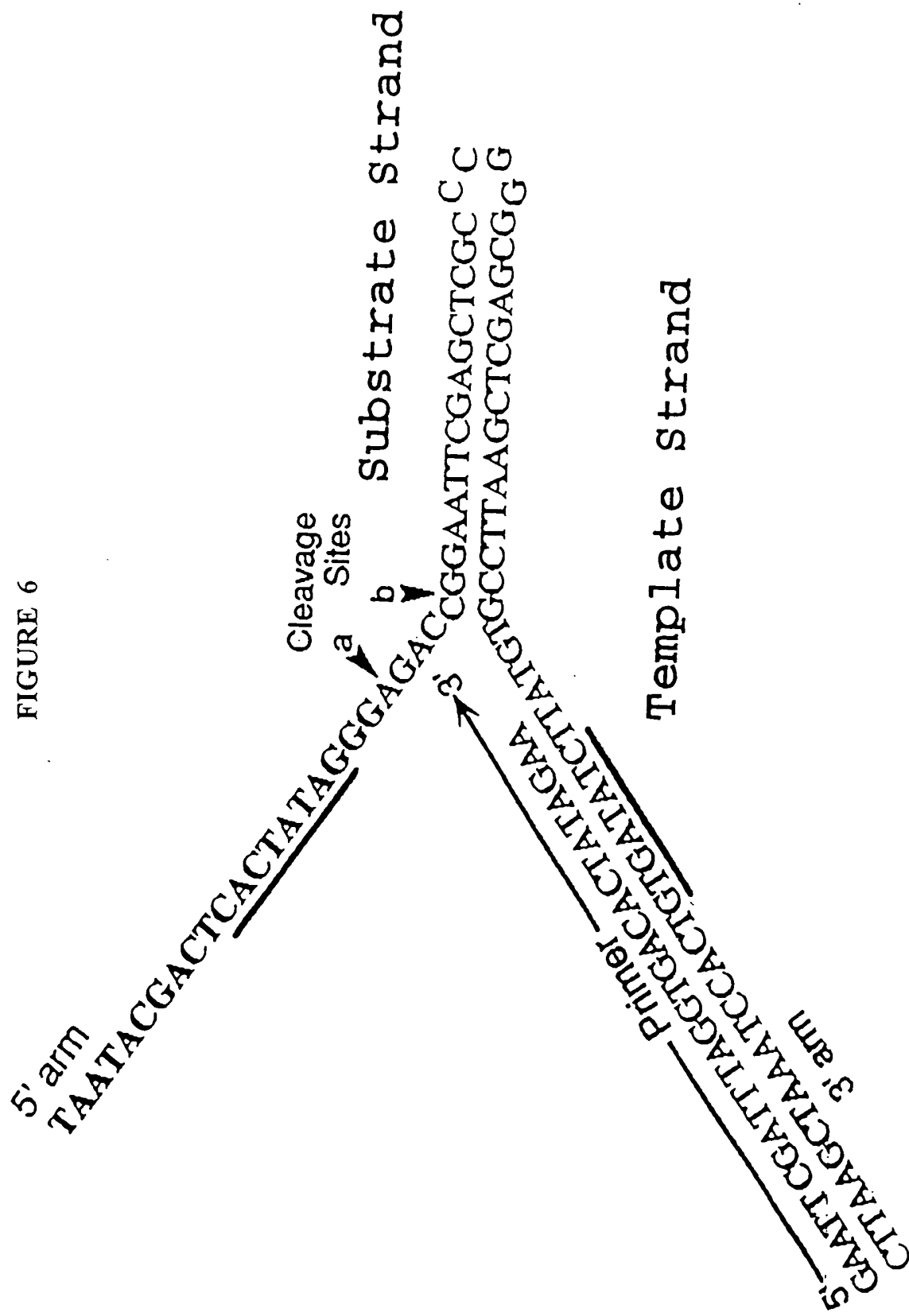


FIGURE 6





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FIGURE 7



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FIGURE 8

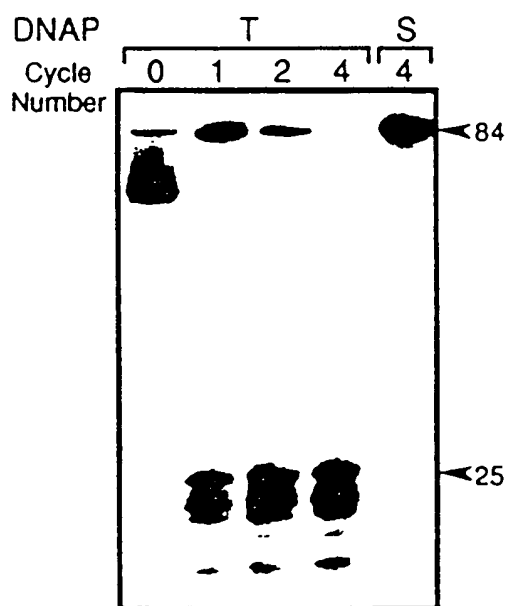
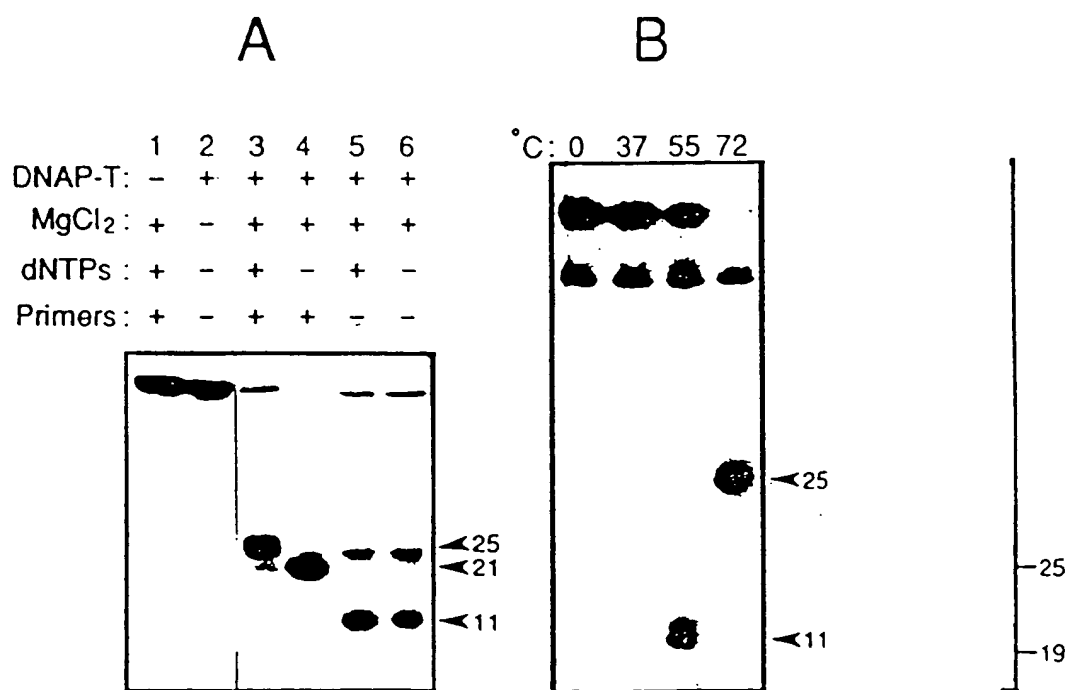


FIGURE 9



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FIGURE 10

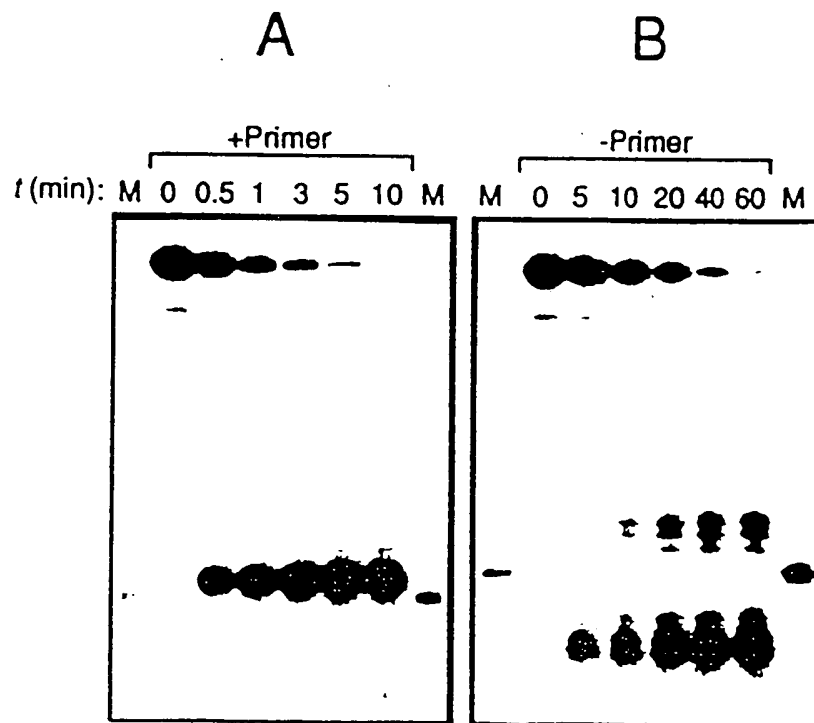


FIGURE 11

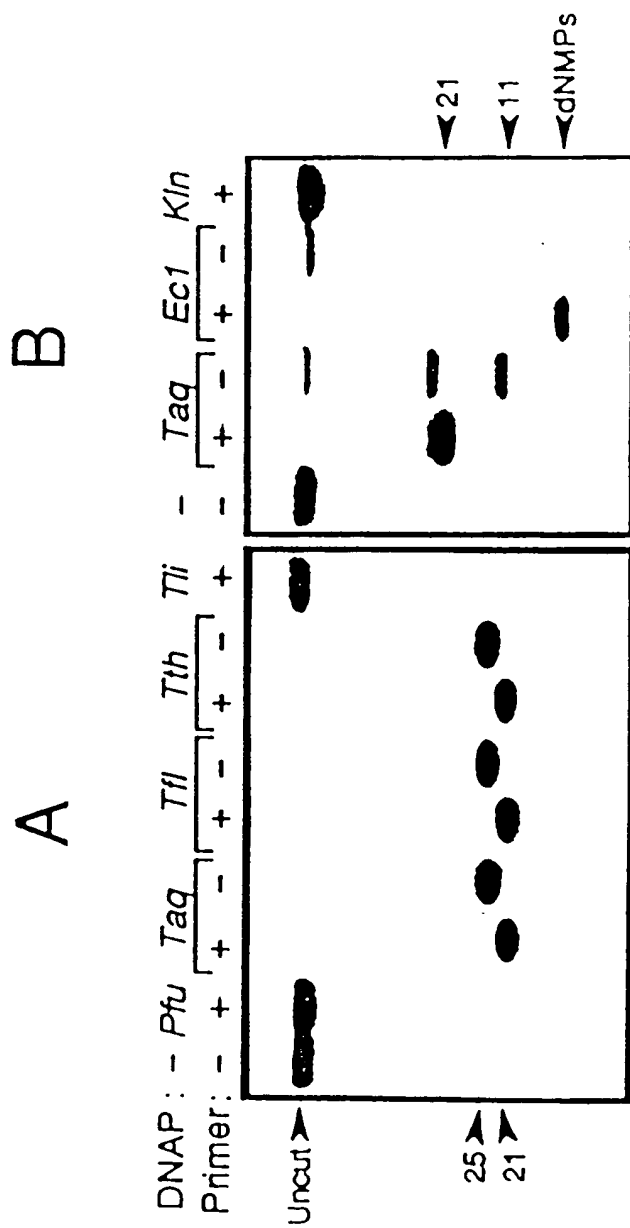


FIGURE 12

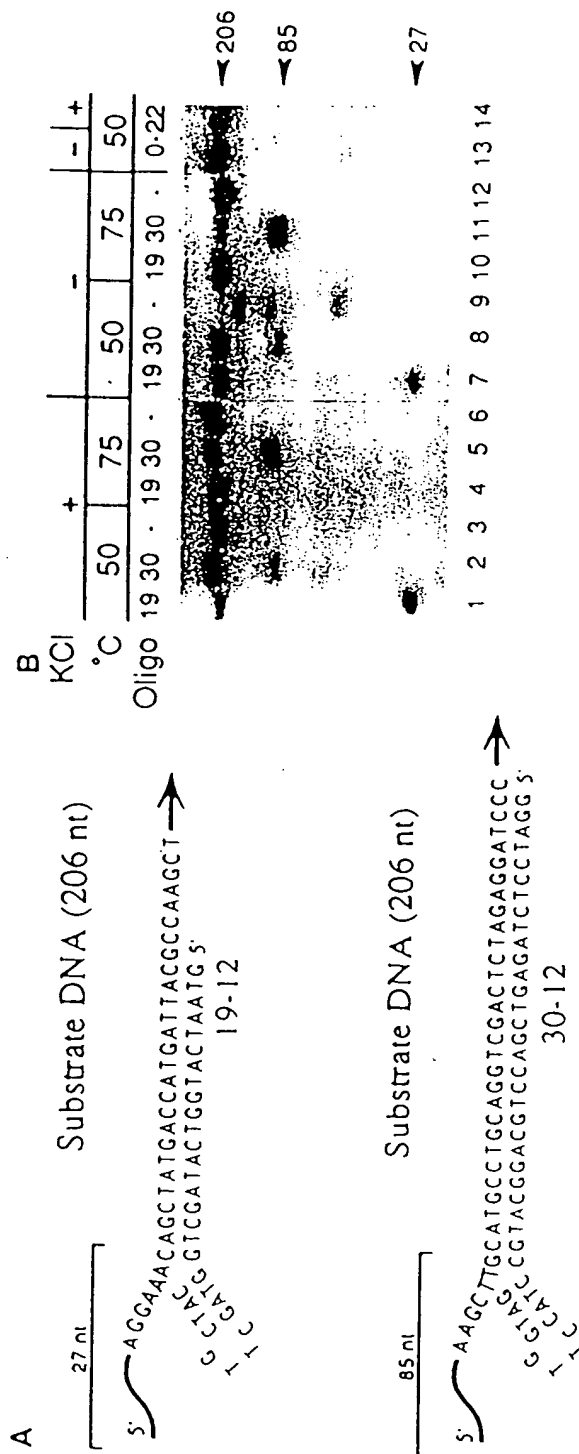


FIGURE 13

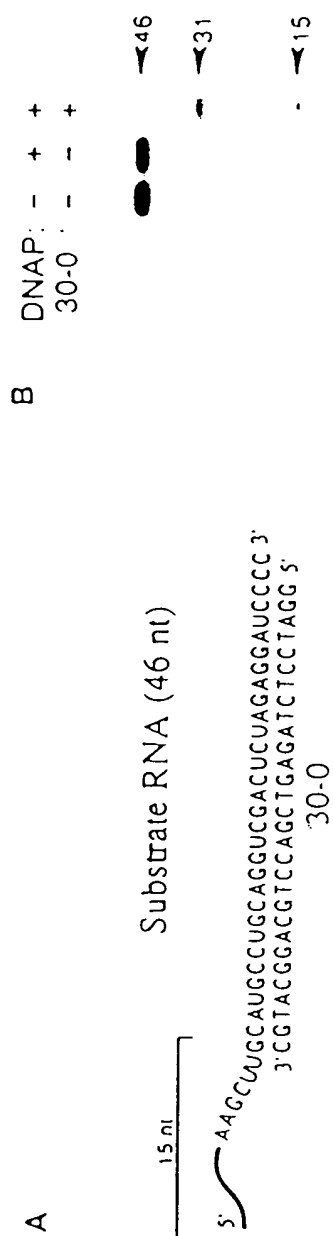


FIGURE 14

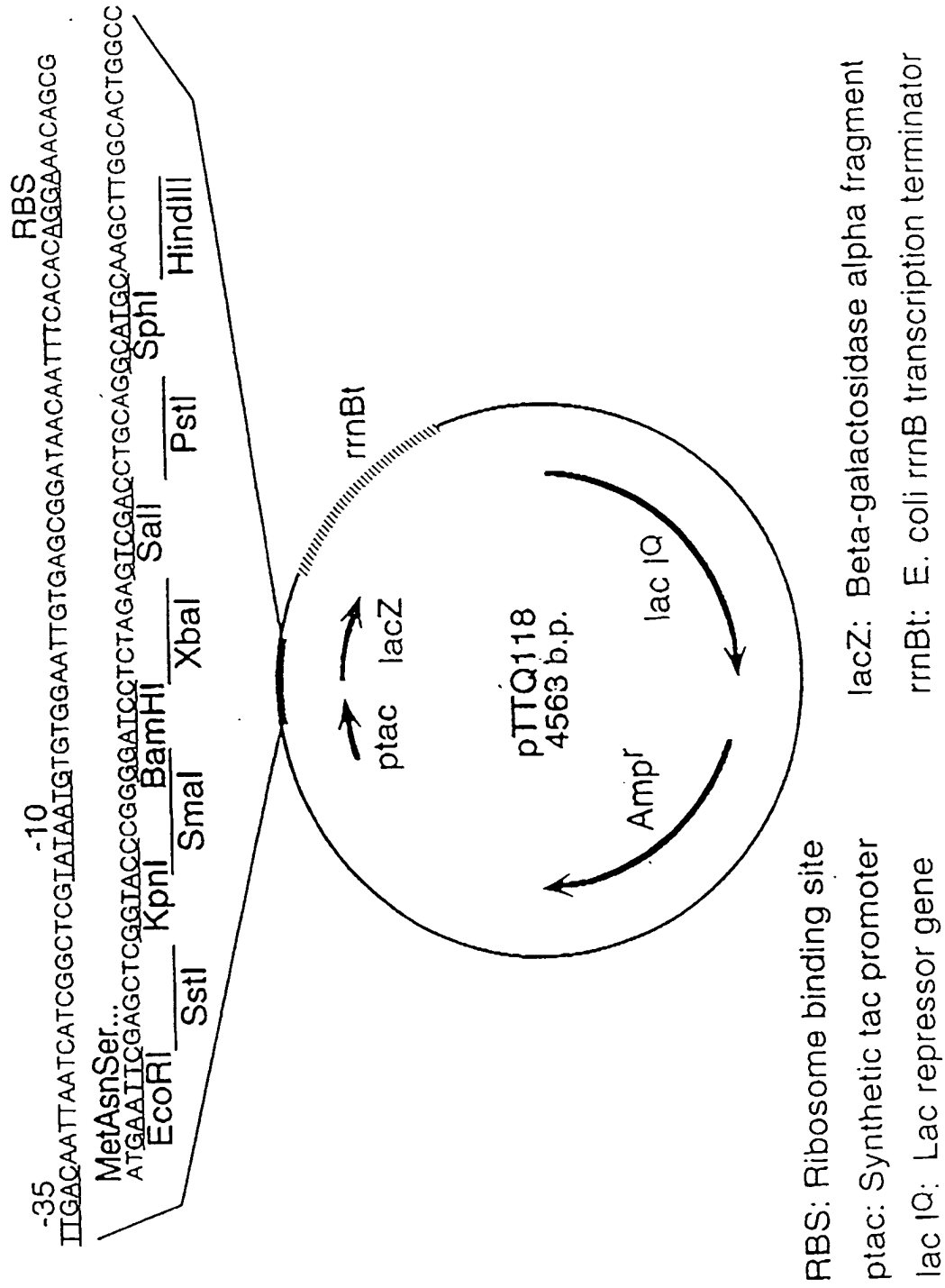
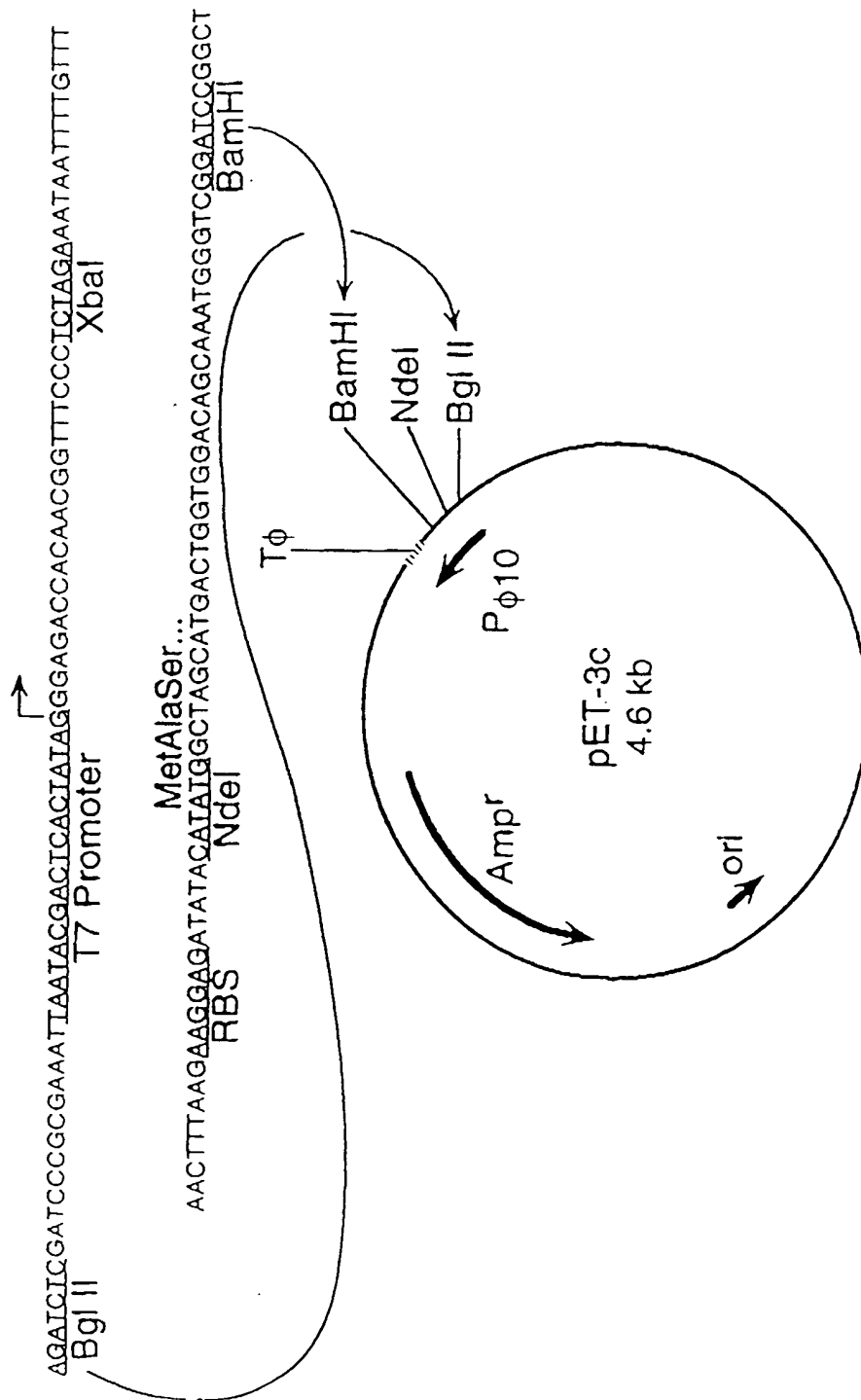




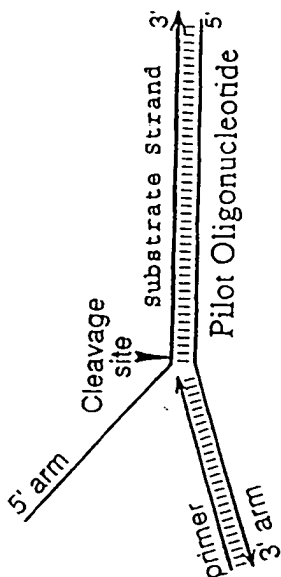
FIGURE 15



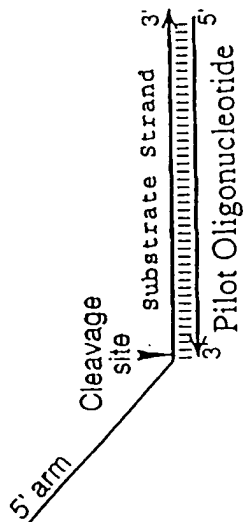
P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter  
Tφ: T7 φ Terminator  
RBS: Ribosome binding site

FIGURE 16

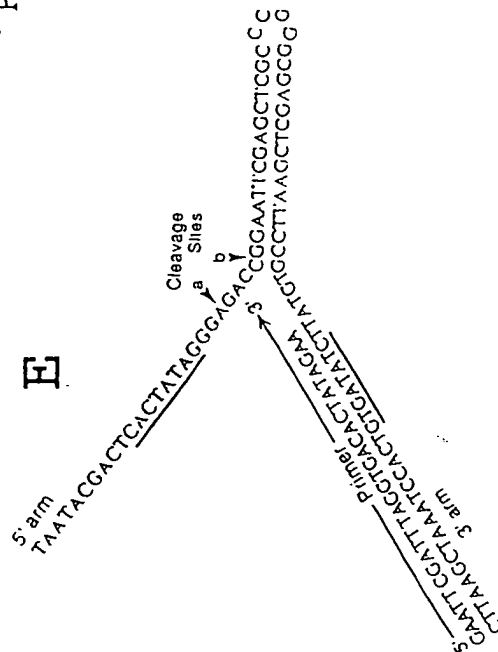
B



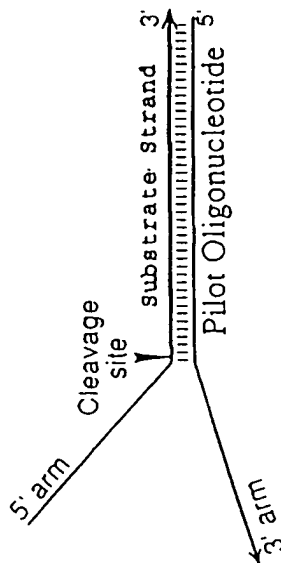
D



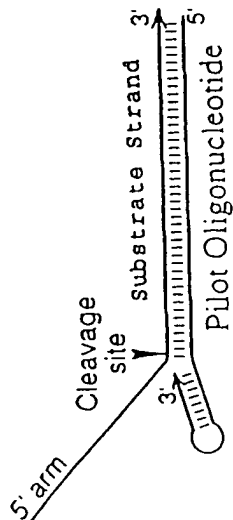
E



A



C



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FIGURE 17

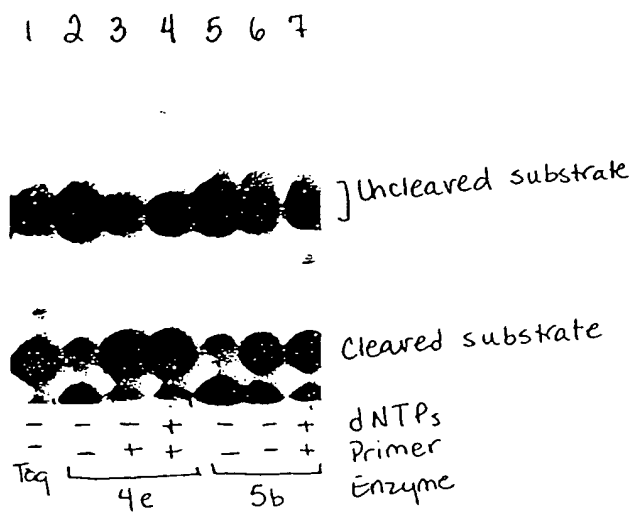
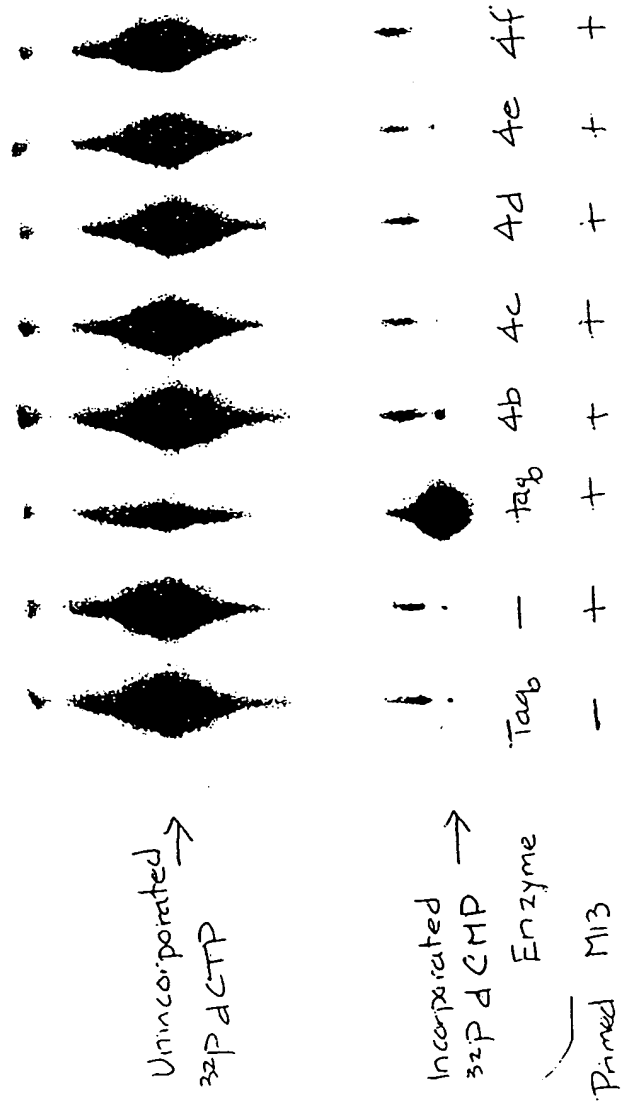


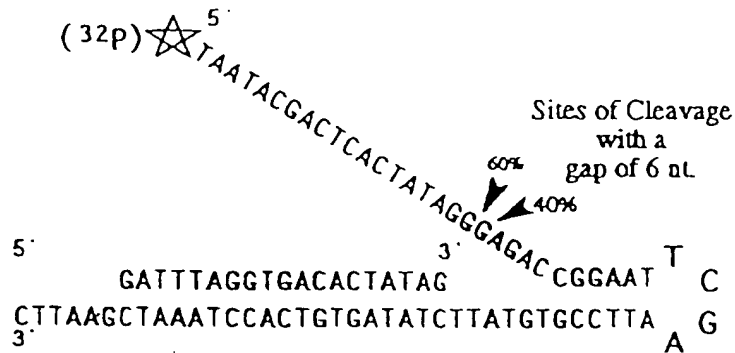
FIGURE 18



10074328.021202


FIGURE 19

A



B

		"4d"		"4b"			
		No Pol. Activity		(2 pt. mutation small activity)		Unmodified DNAP Tag	
1	2	3	4	5	6	7	8
		C <sup>+</sup>		pTag <sup>+</sup>		Tag <sup>+</sup>	
		+		+		+	

84 nt —  ← hairpin test molecule  
← conversion to double stranded.  
(complete extension of primer)


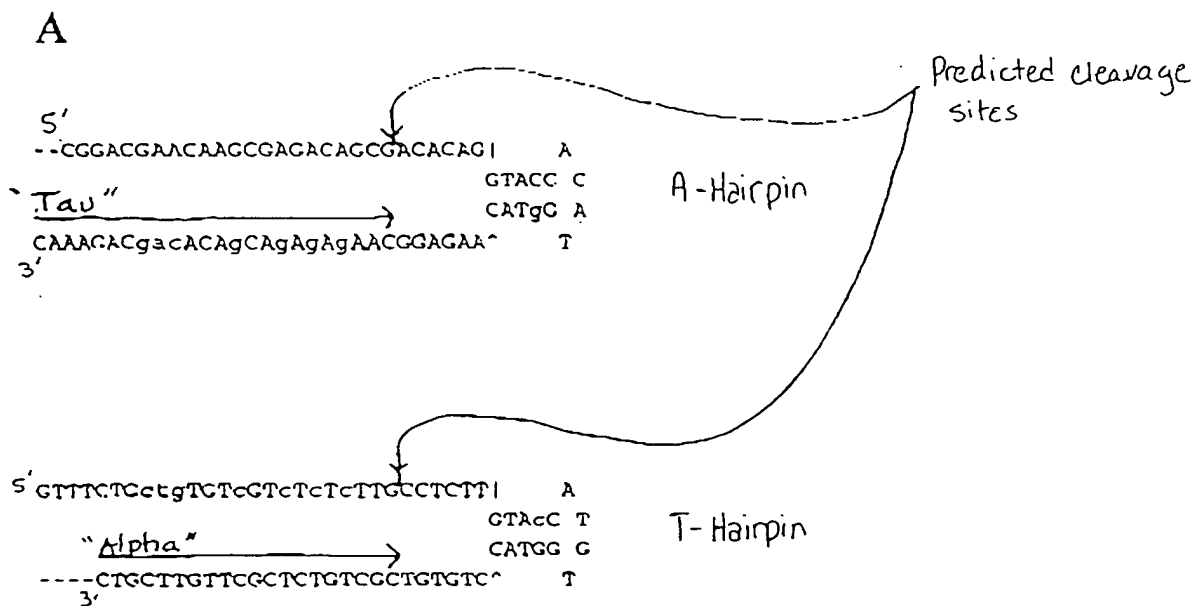
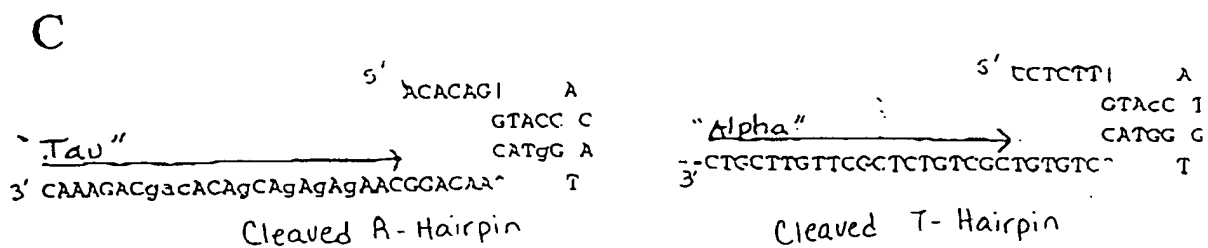
desired product 21 nuc. →  } Multiple bands caused by polymerization  
↑ some aberrant cleavage with "4b" because of residual polymerase activity.

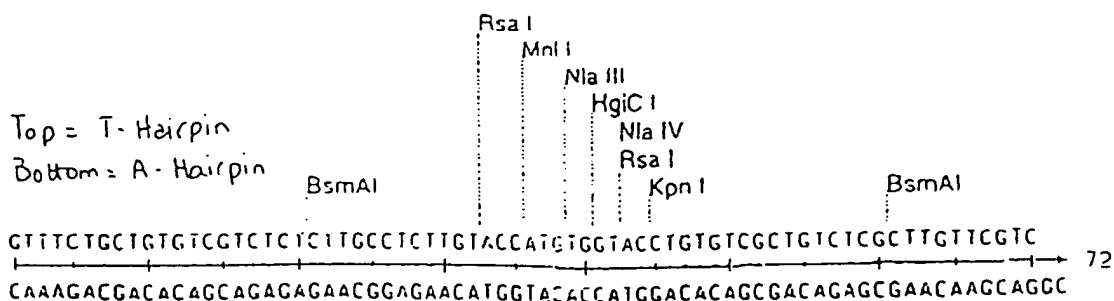
FIGURE 20



**B** Sequence of alpha primer:  
 5' GAC GAA CAA CGG AGA CAG CG 3'



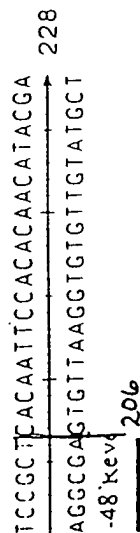
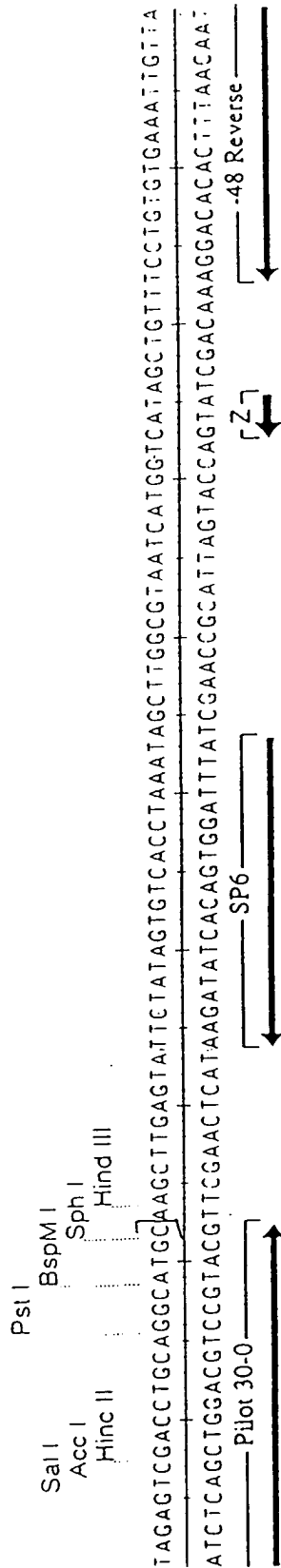
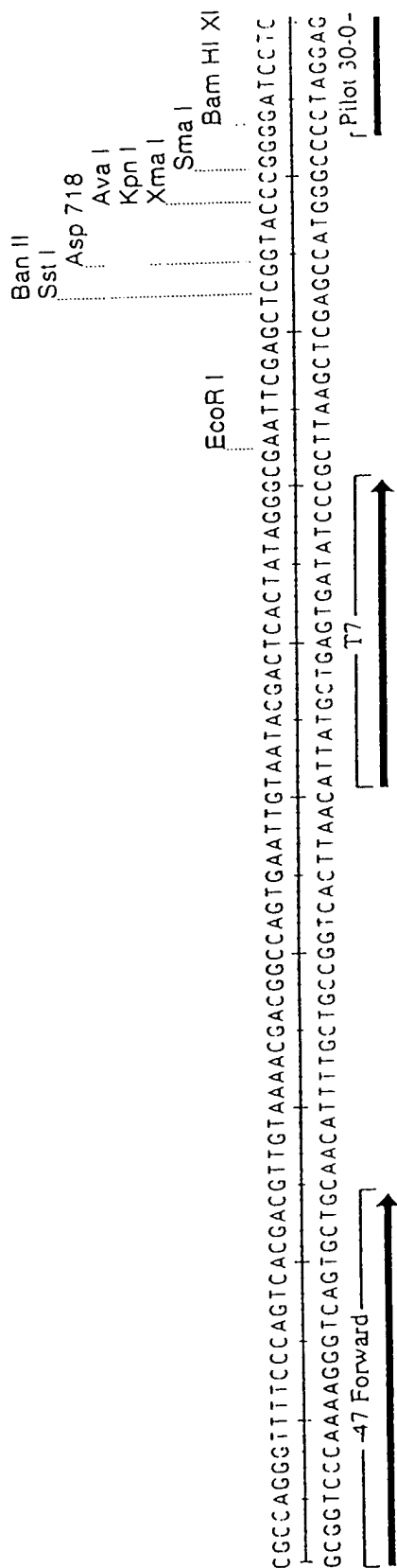
**D**



30

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FIGURE 21



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FIGURE 22A

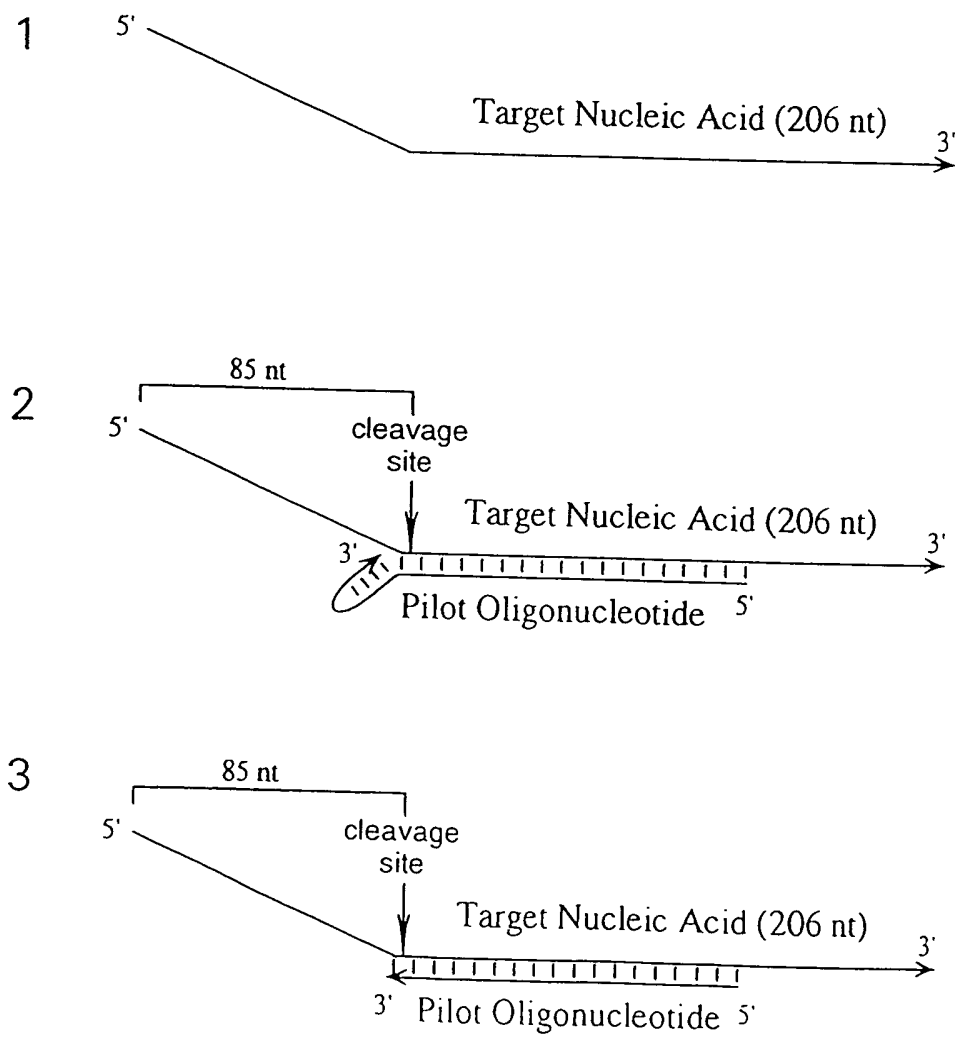




FIGURE 22B

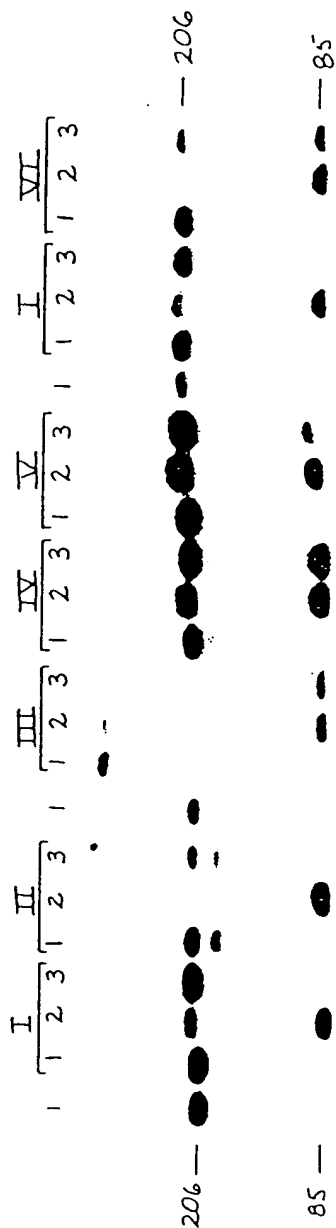
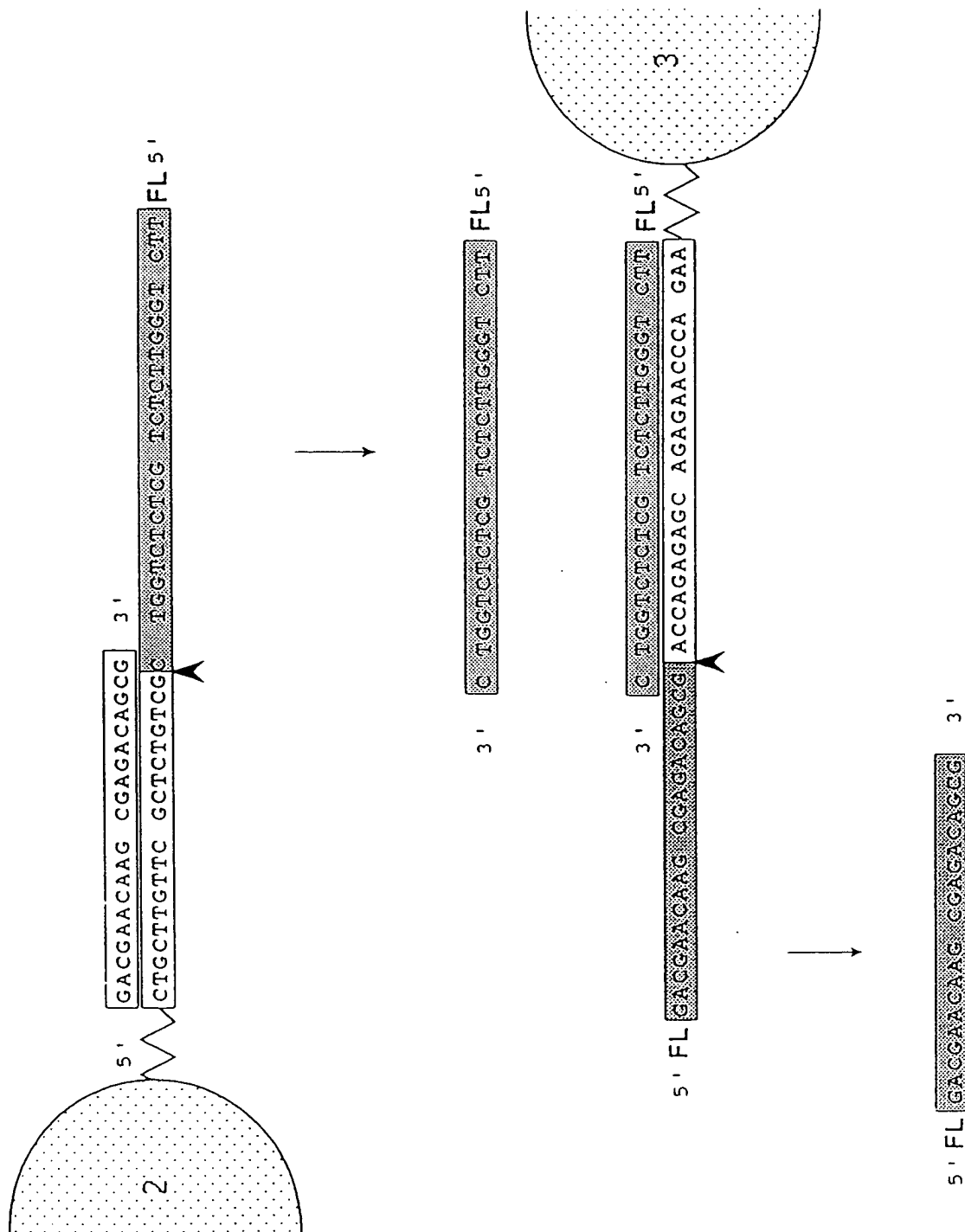
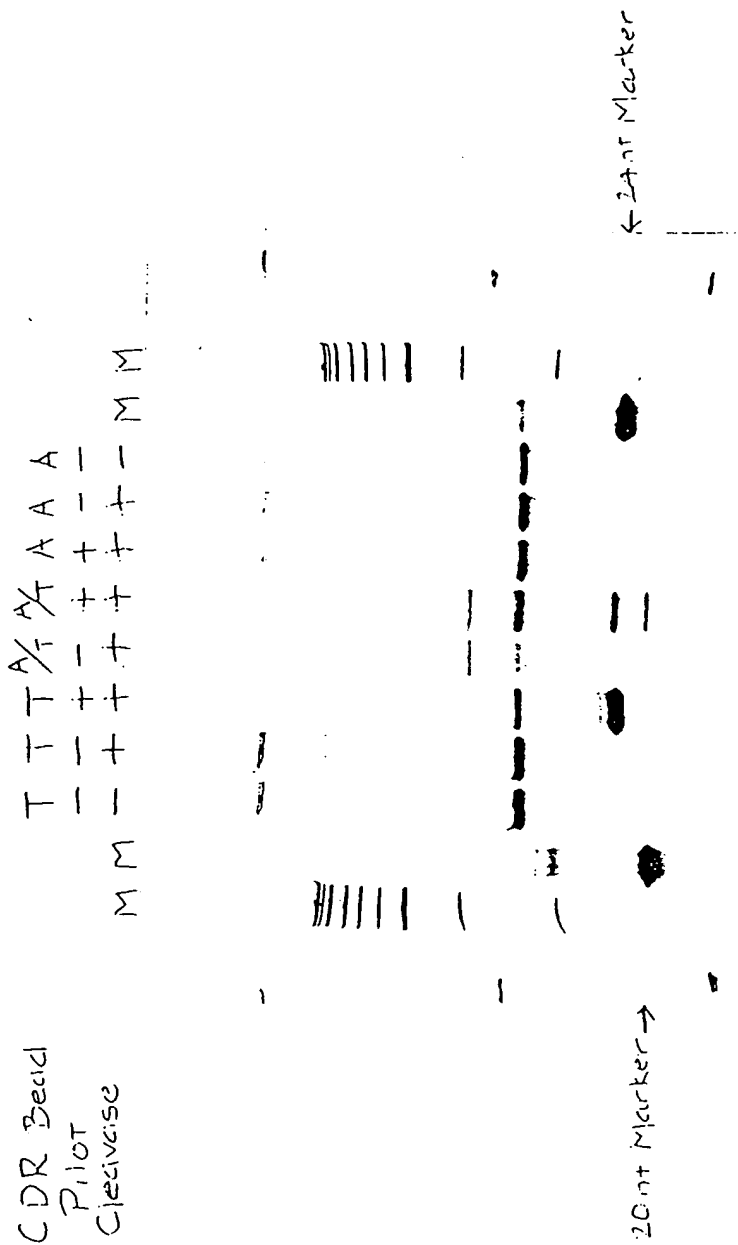


FIGURE 23



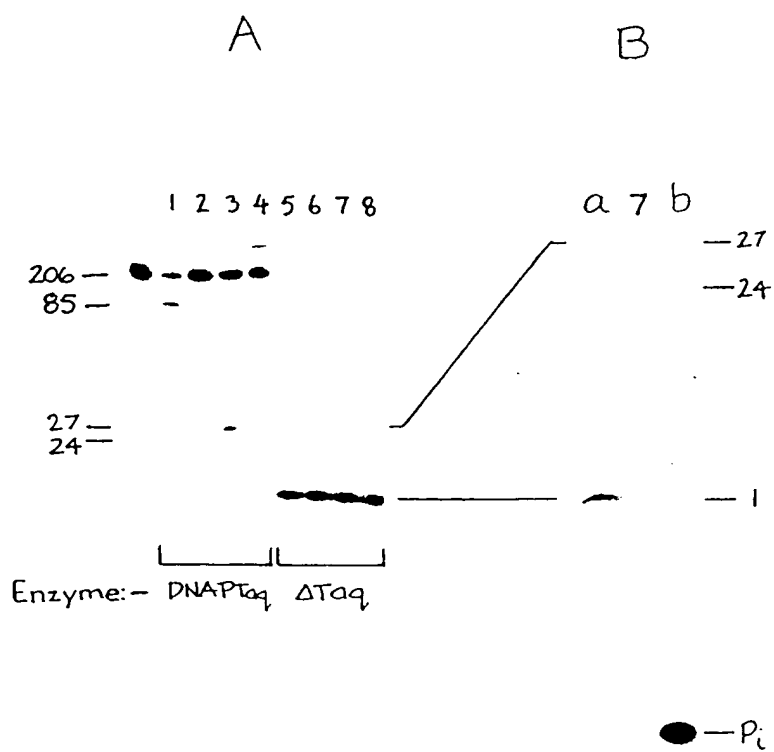
202720" 82E42007

FIGURE 24



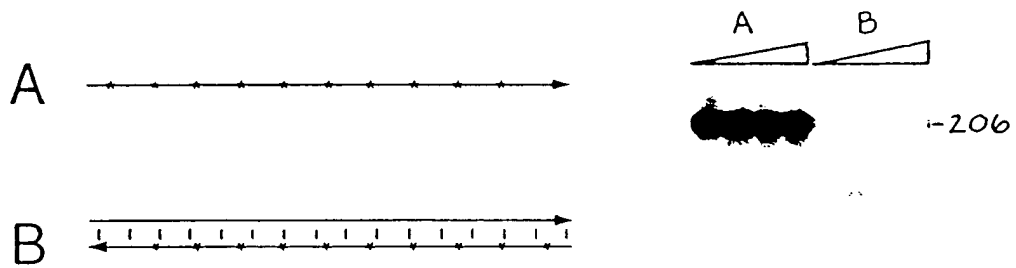
202120" B2E4/001

FIGURE 25



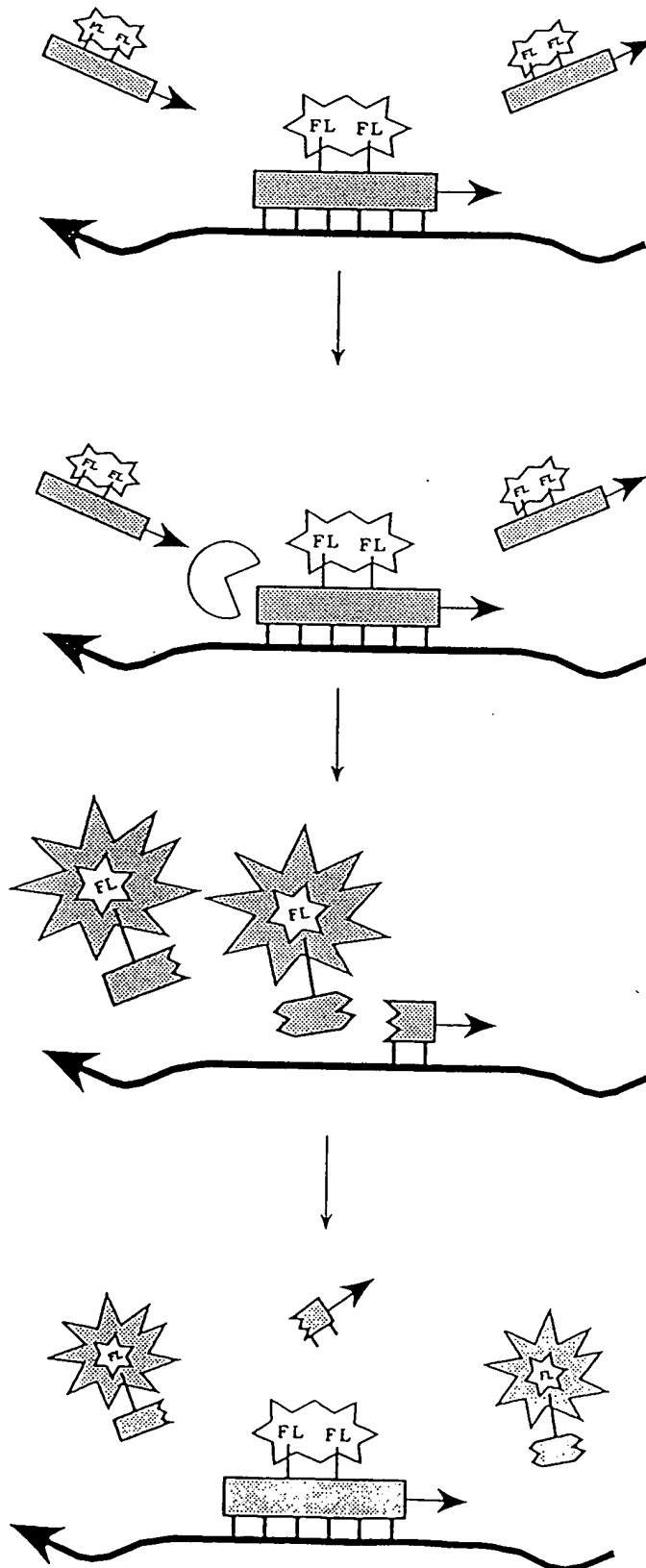
10074328-021202

FIGURE 26



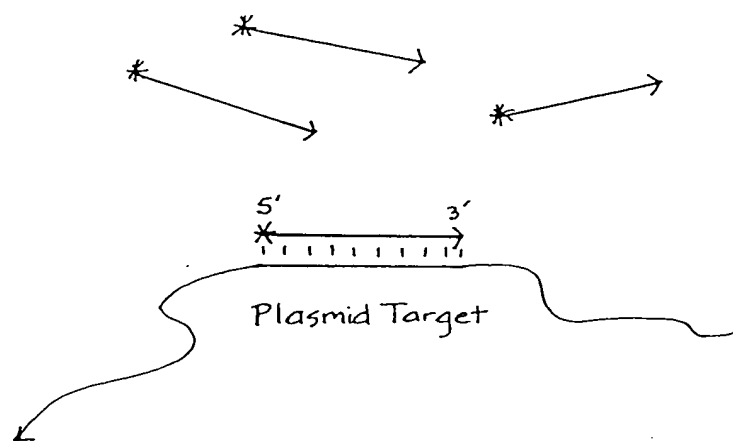
\* =  $^{32}\text{P}$

FIGURE 27



10074328.021202

FIGURE 28A



\* =  $^{32}\text{P}$  5' terminal phosphate

2021220" 8254007

FIGURE 28B

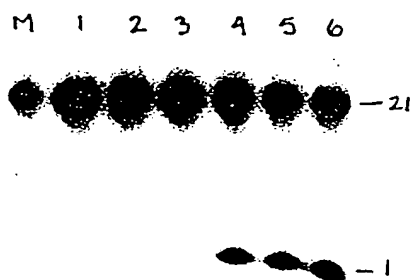




FIGURE 29

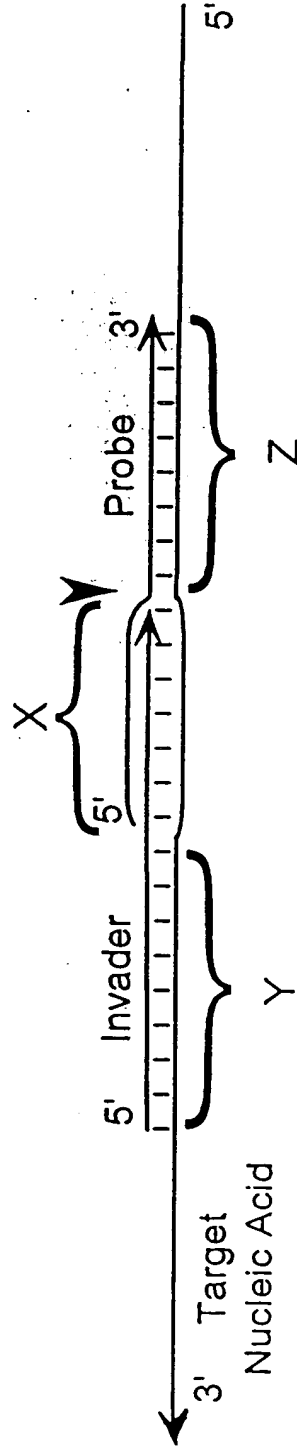
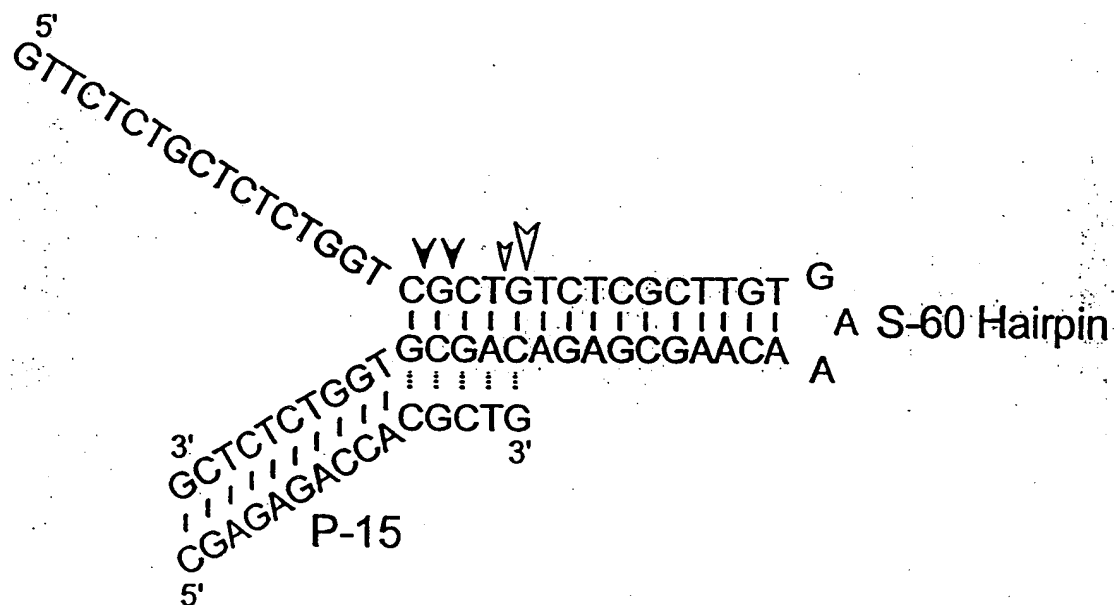
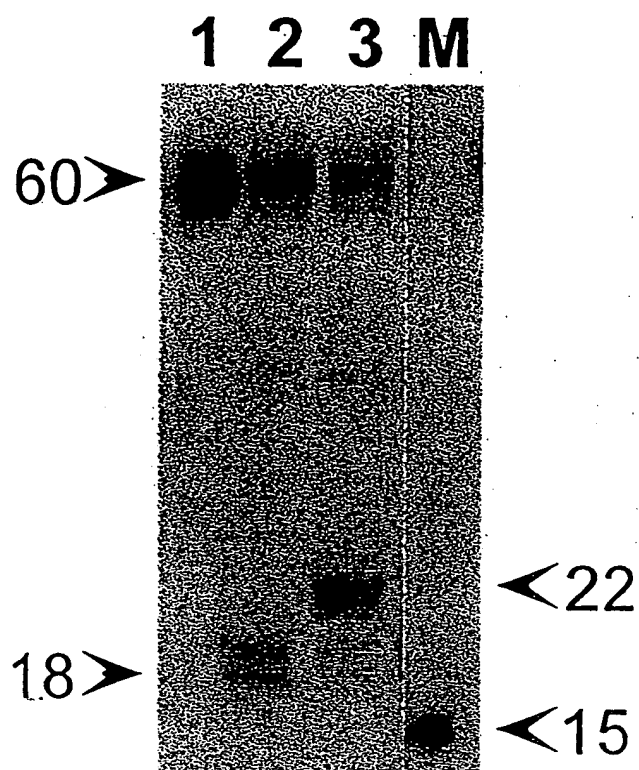


FIGURE 30



10074328 031203

FIGURE 31



202120" 82E4C00T

FIGURE 32  
202120" BEEH200T

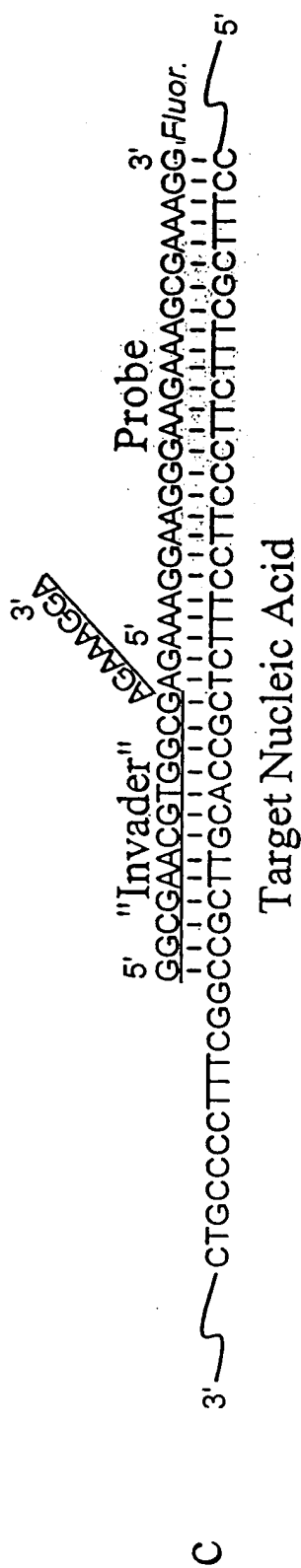
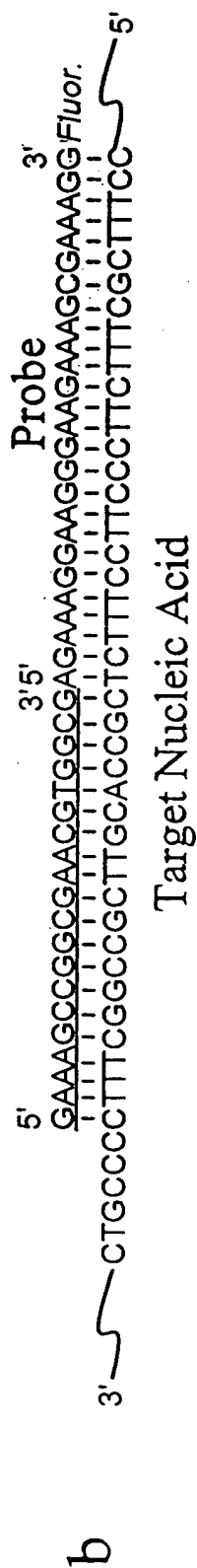
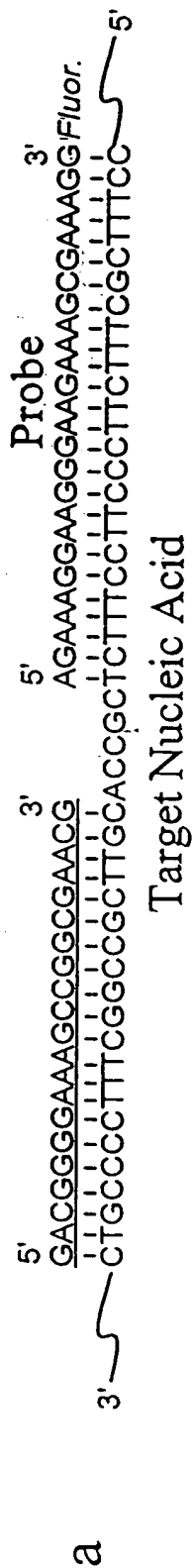
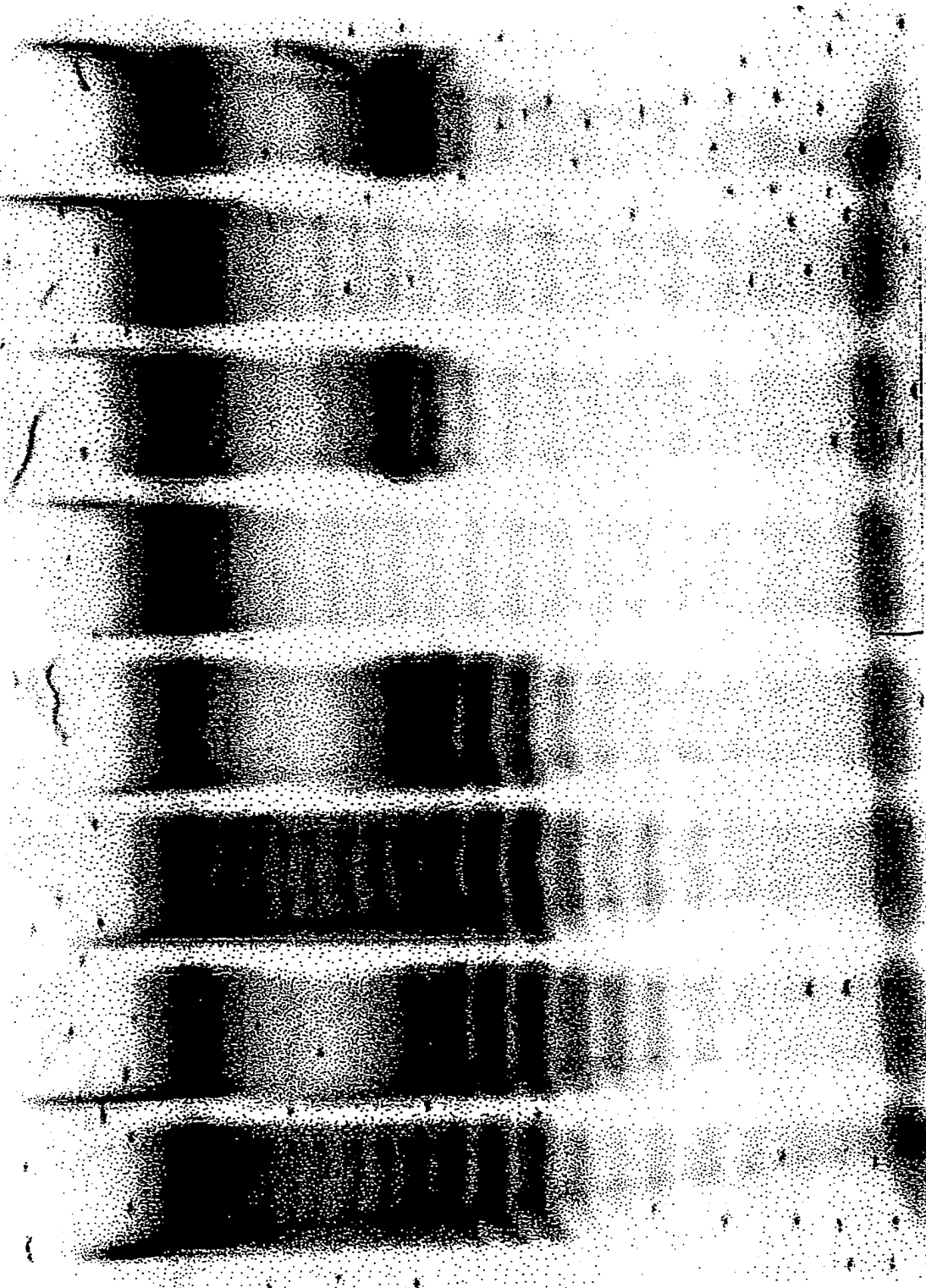


FIGURE 33

202T20" 82EH/001

1 2 3 4 5 6 7 8



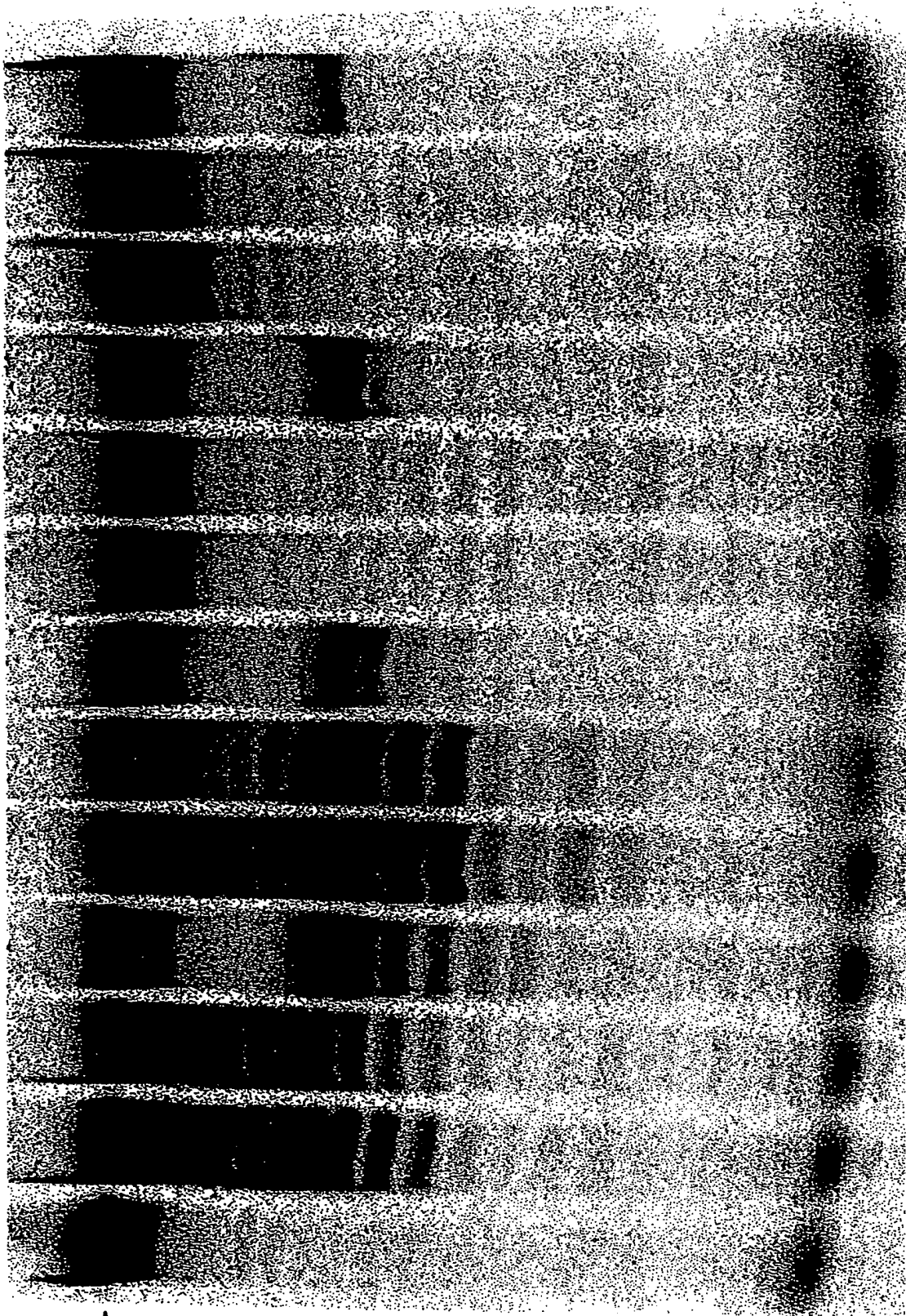
26>

45

FIGURE 34

202120" 82E4200T

M 1 2 3 4 5 6 7 8 9 10 11 12



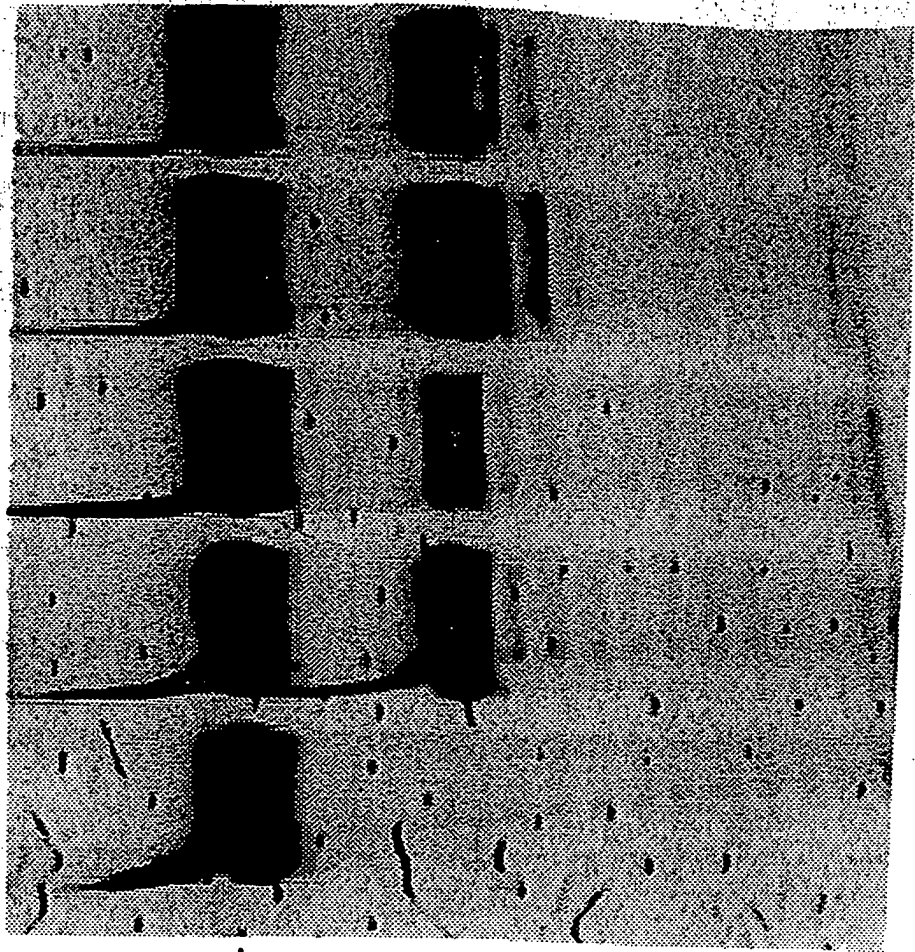
26

46

FIGURE 35

202T20" B2EH/00T

1 2 3 4 5



26

FIGURE 36  
202120 BEEH/001

M 1 2 3 4 5 6 7 8 9 10 11 12 13

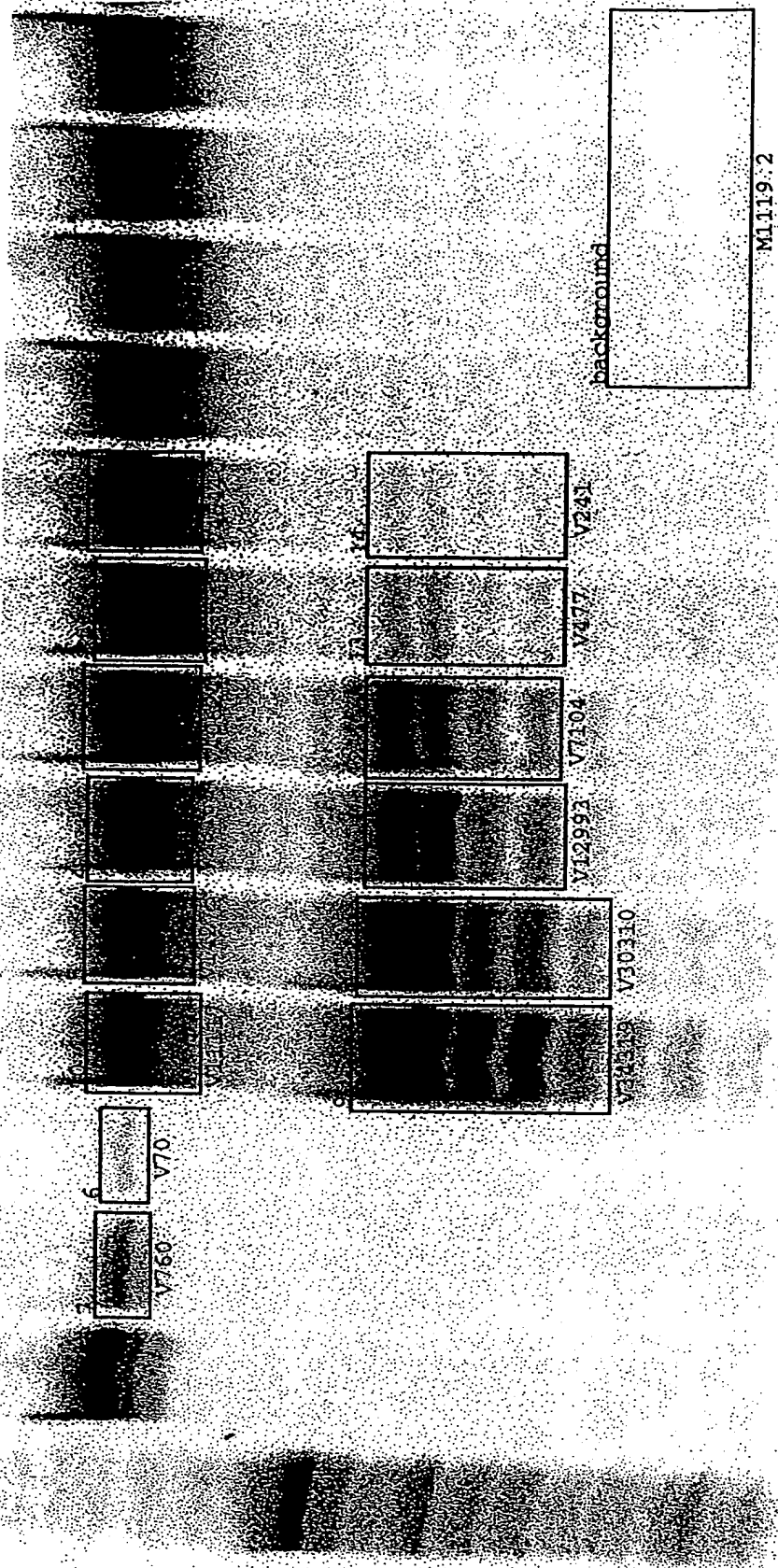




FIGURE 37

202120" B2E4700F

1 2 3 4 5 6 7 8 9 10 11

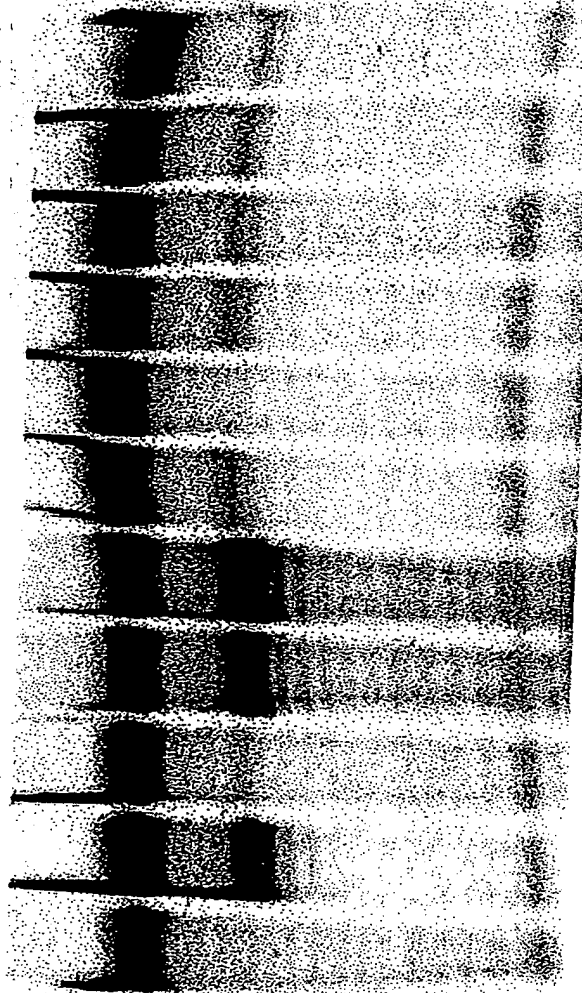


FIGURE 38 B2E47001

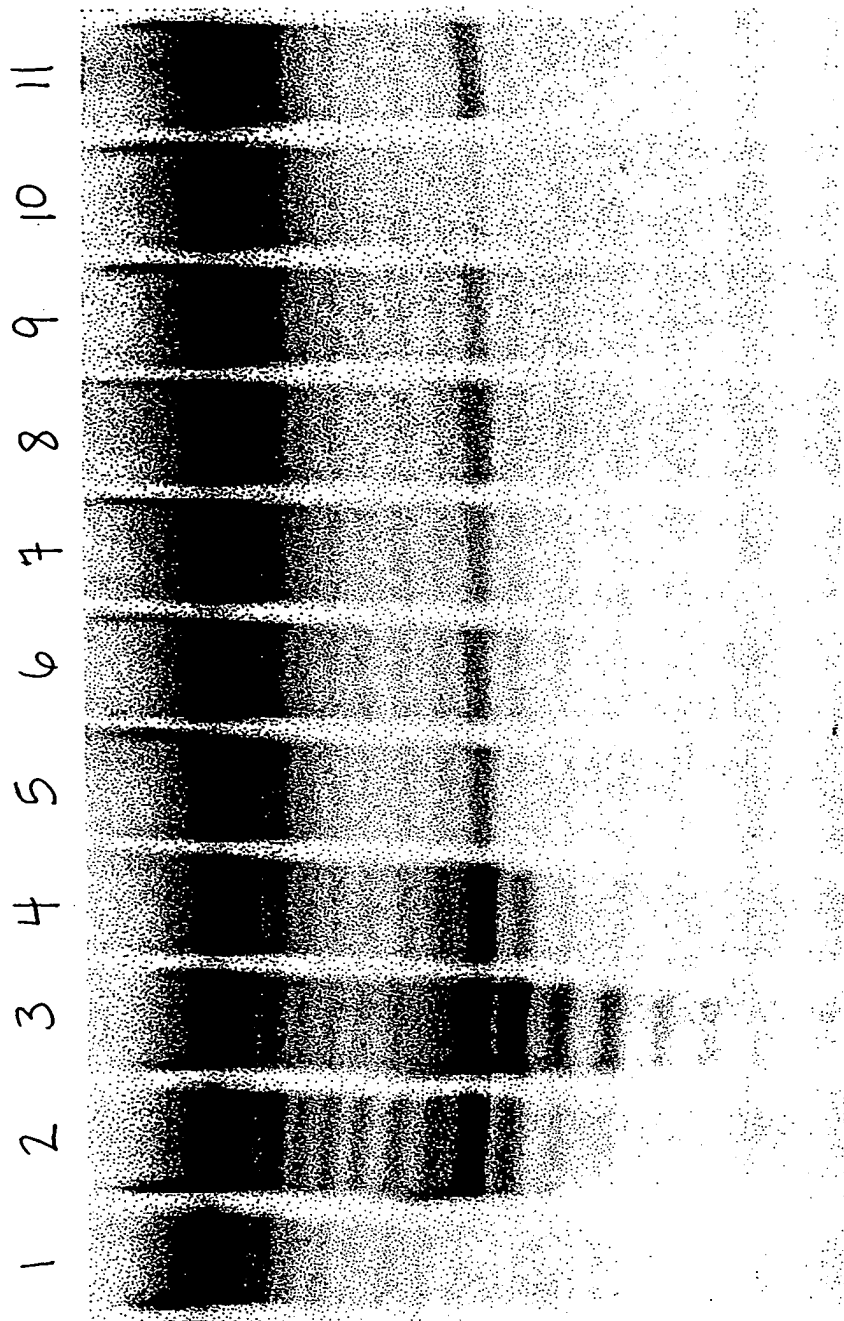
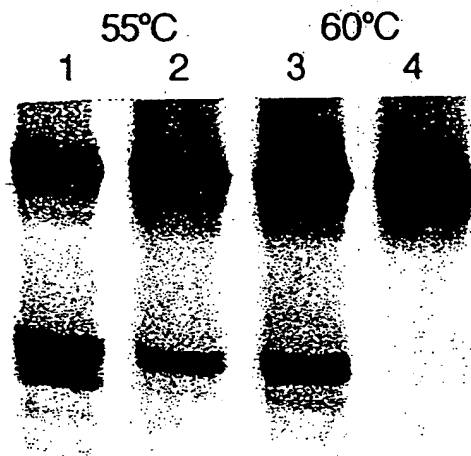
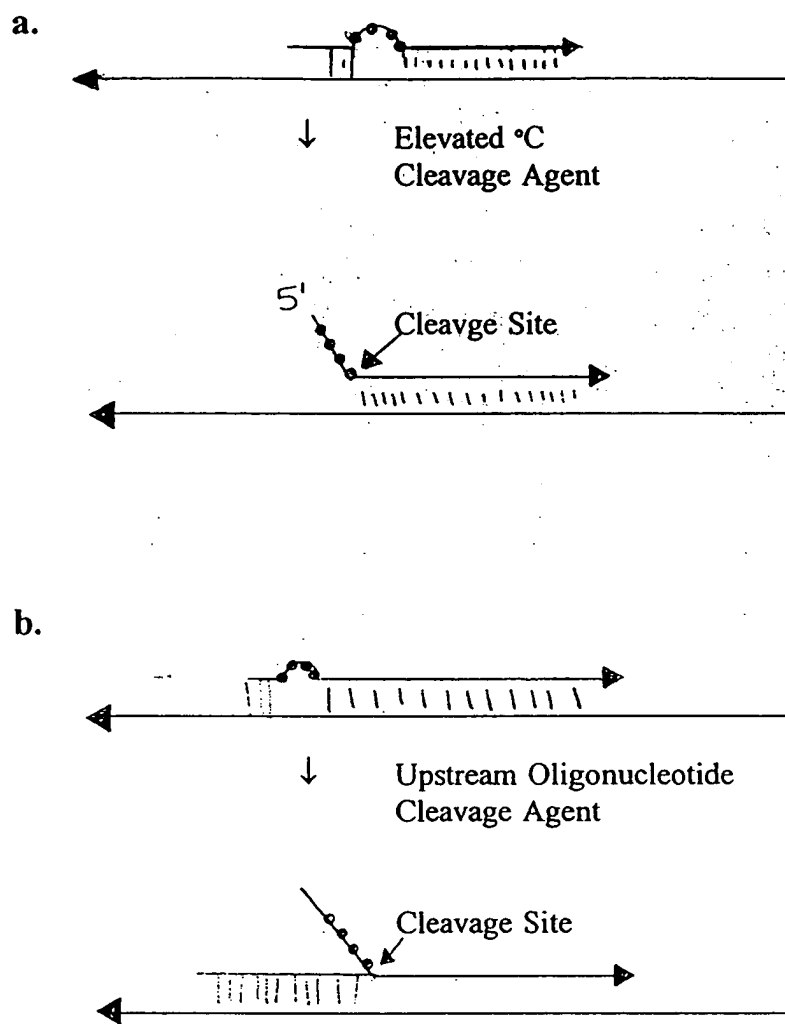


FIGURE 39



20212018254001

FIGURE 40



10074328 021202

202120" 82E42001

FIGURE 41

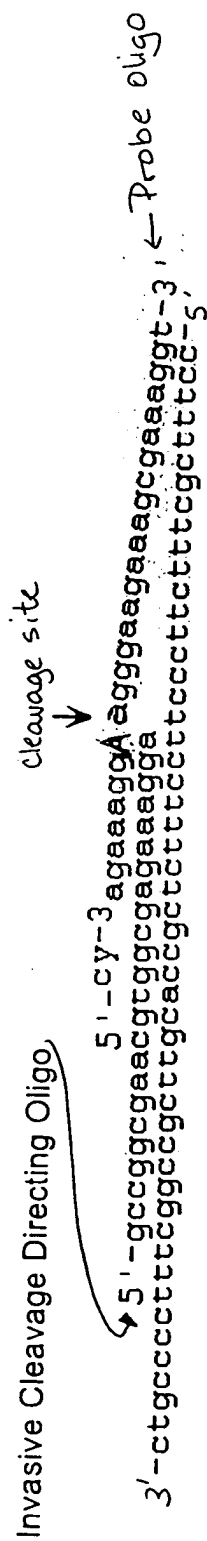
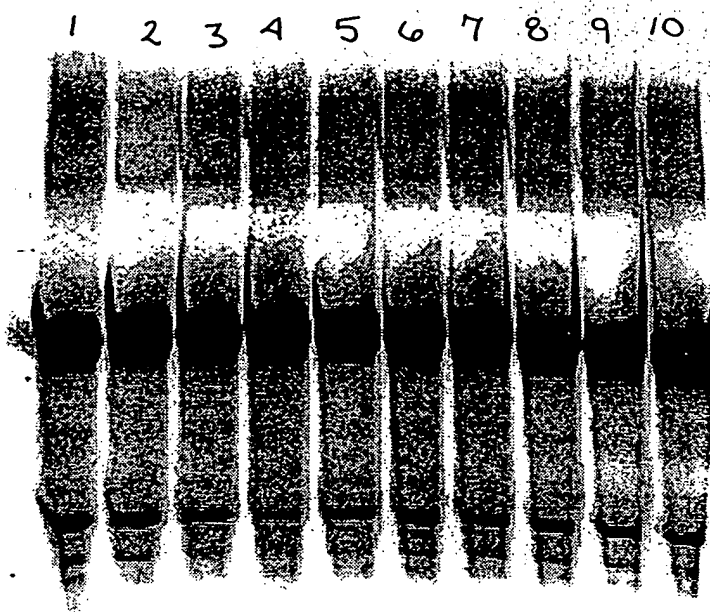


FIGURE 42



10074328.021202

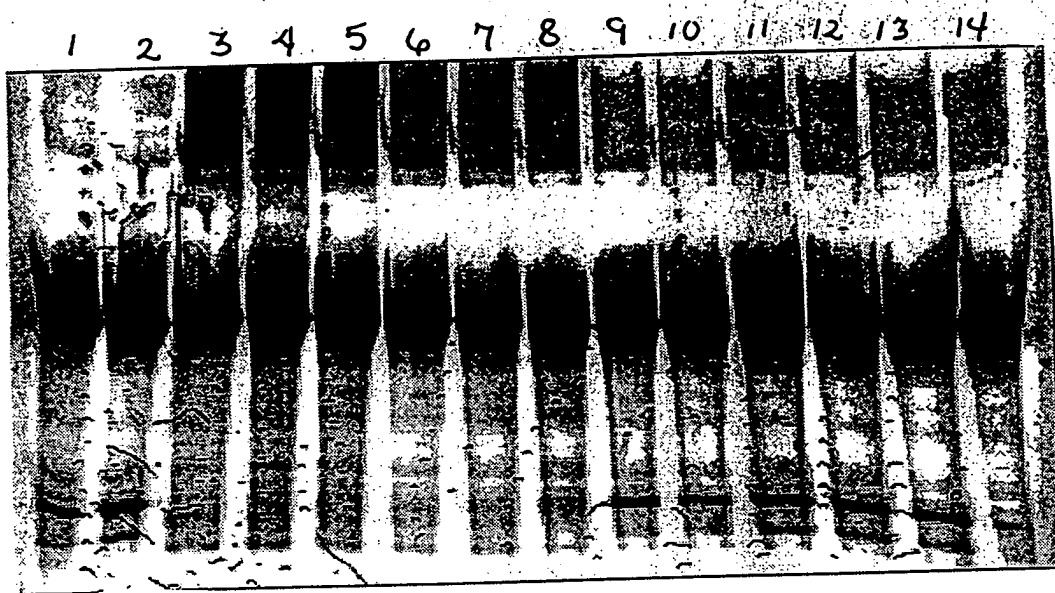
FIGURE 43



10074328 .021202

SS

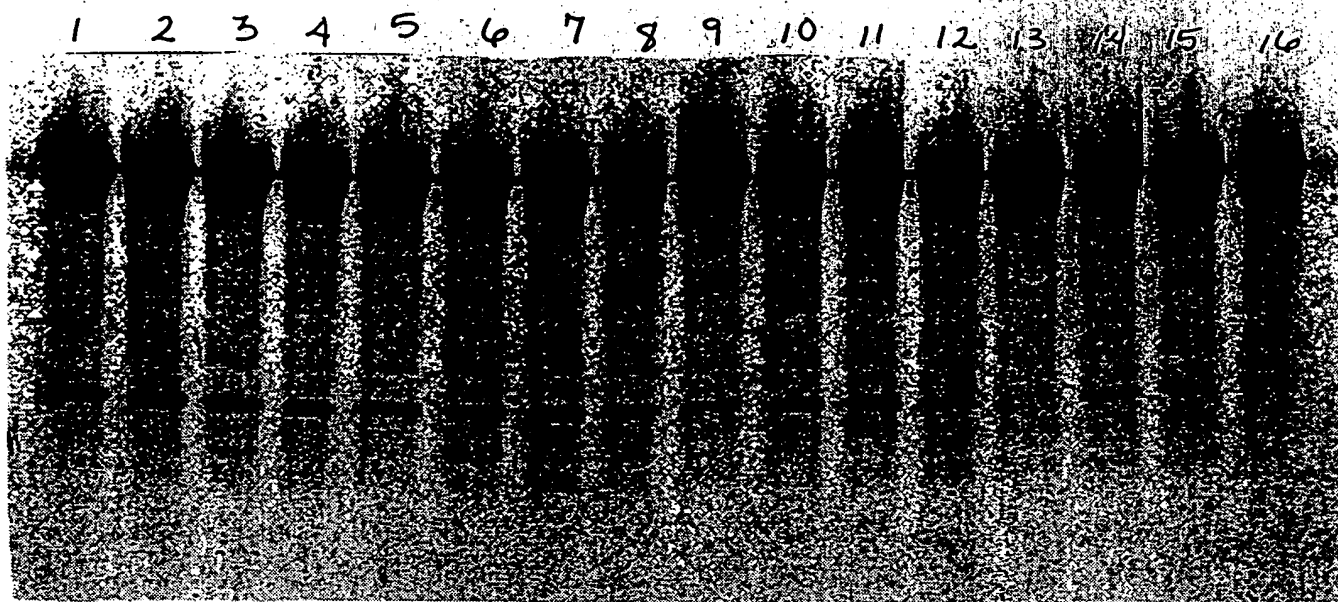
FIGURE 44



10074328 021202



FIGURE 45



10074328-021202

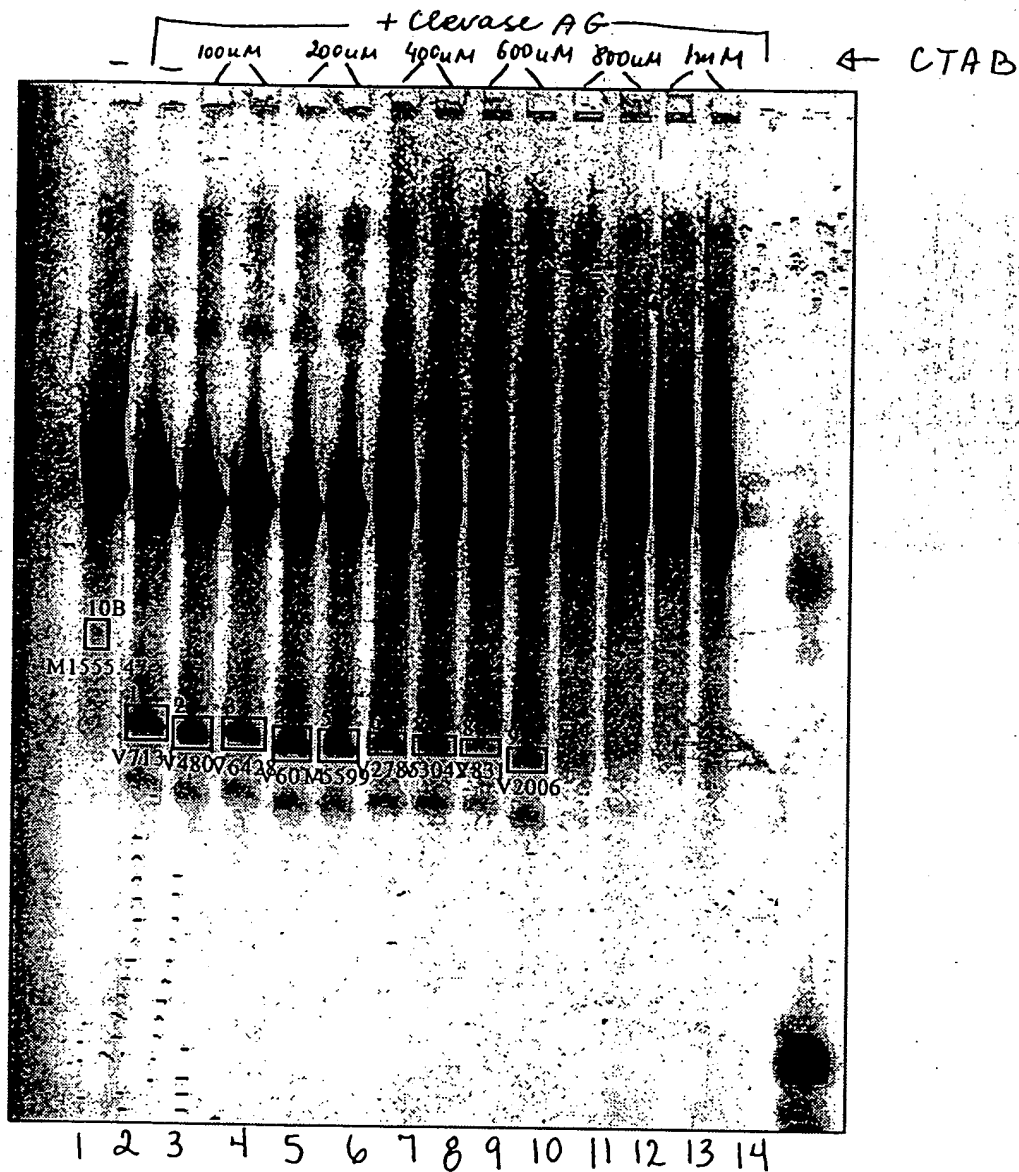
FIGURE 46



10074328.021202

58

FIGURE 47



10074328.021202

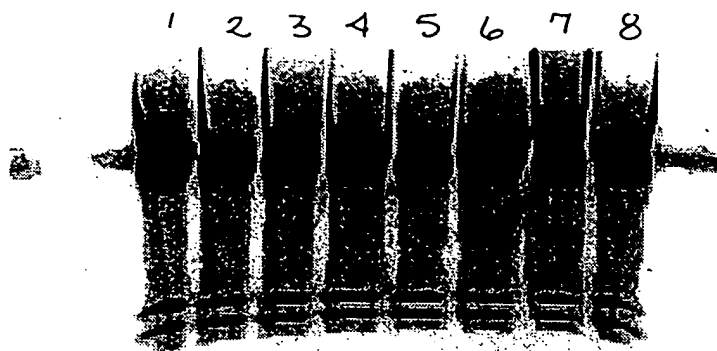
59

FIGURE 48



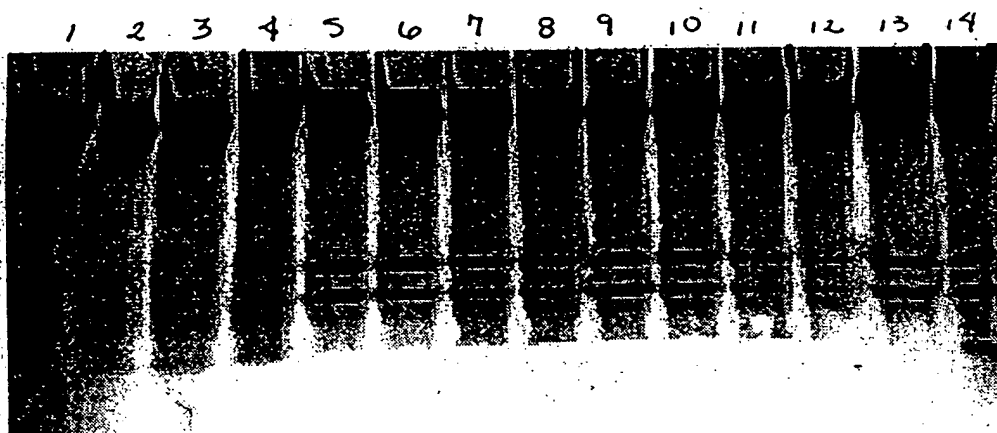
202120" B2E4200T

FIGURE 49



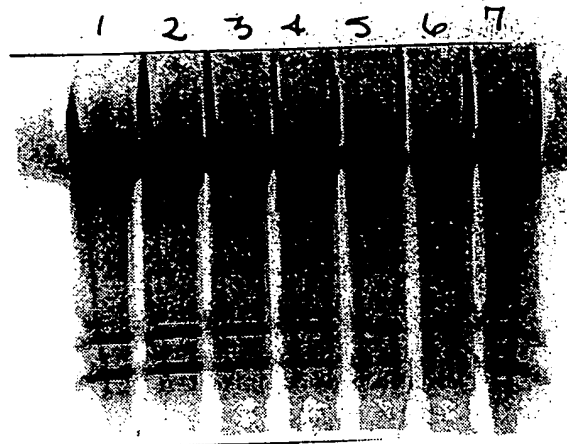
10074328.024303  
202120" B2E7/001

FIGURE 50



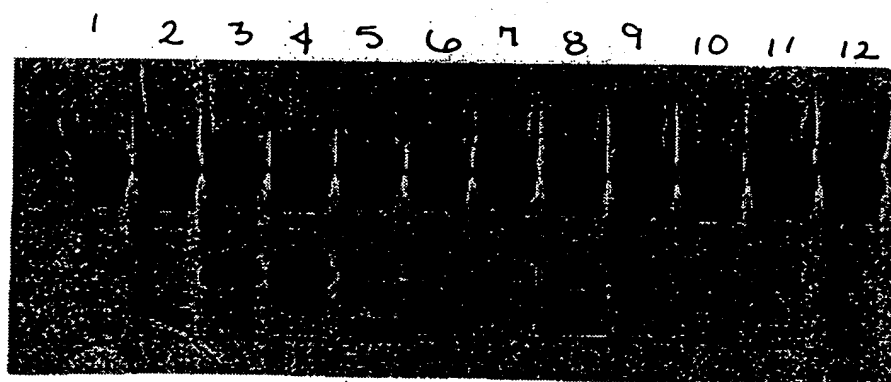
202120" 32E42001

FIGURE 51



10074328 021202

FIGURE 52



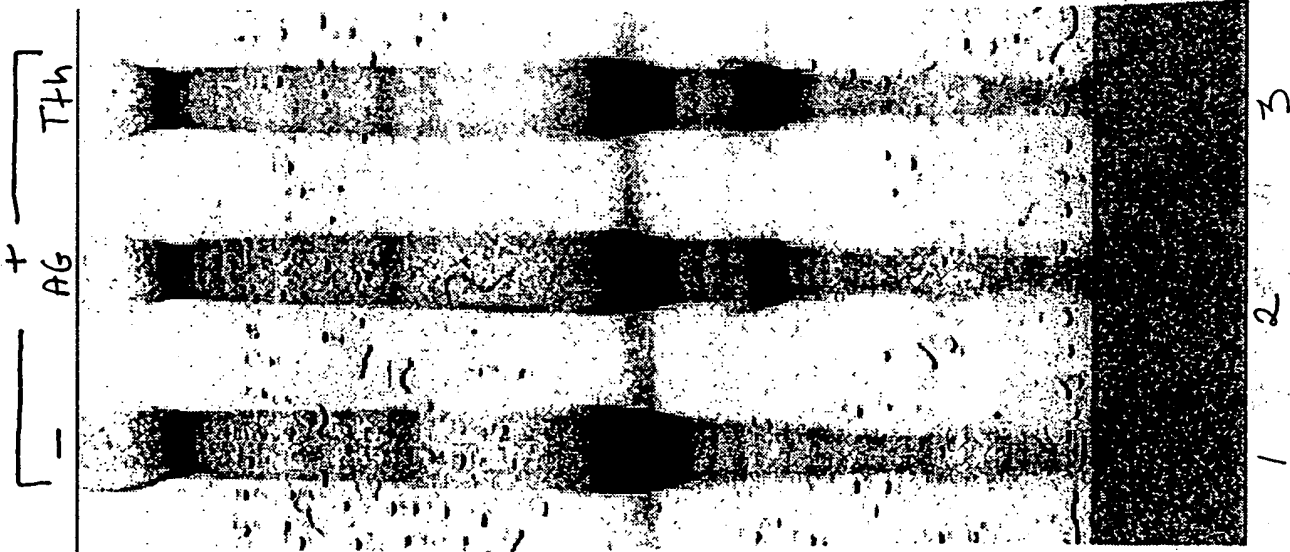
10074323.021202

64



FIGURE 53241.001

a



TARGET RNA →

UNCLEAVED  
PROBE →

CLEAVED  
PROBE →

65

b

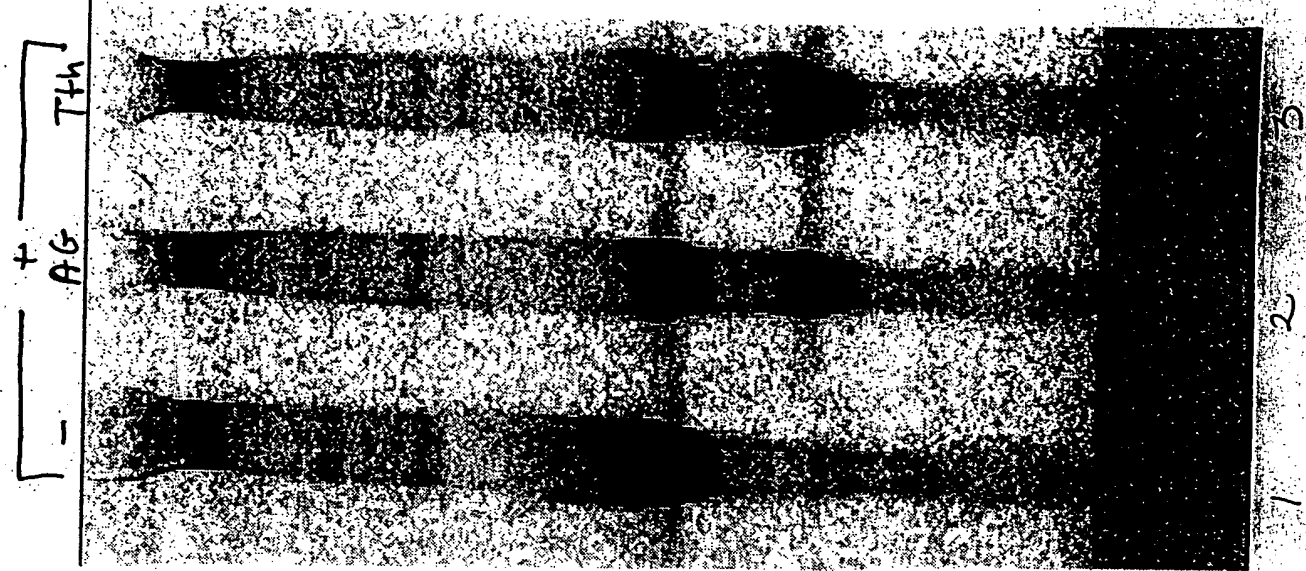


FIGURE 54

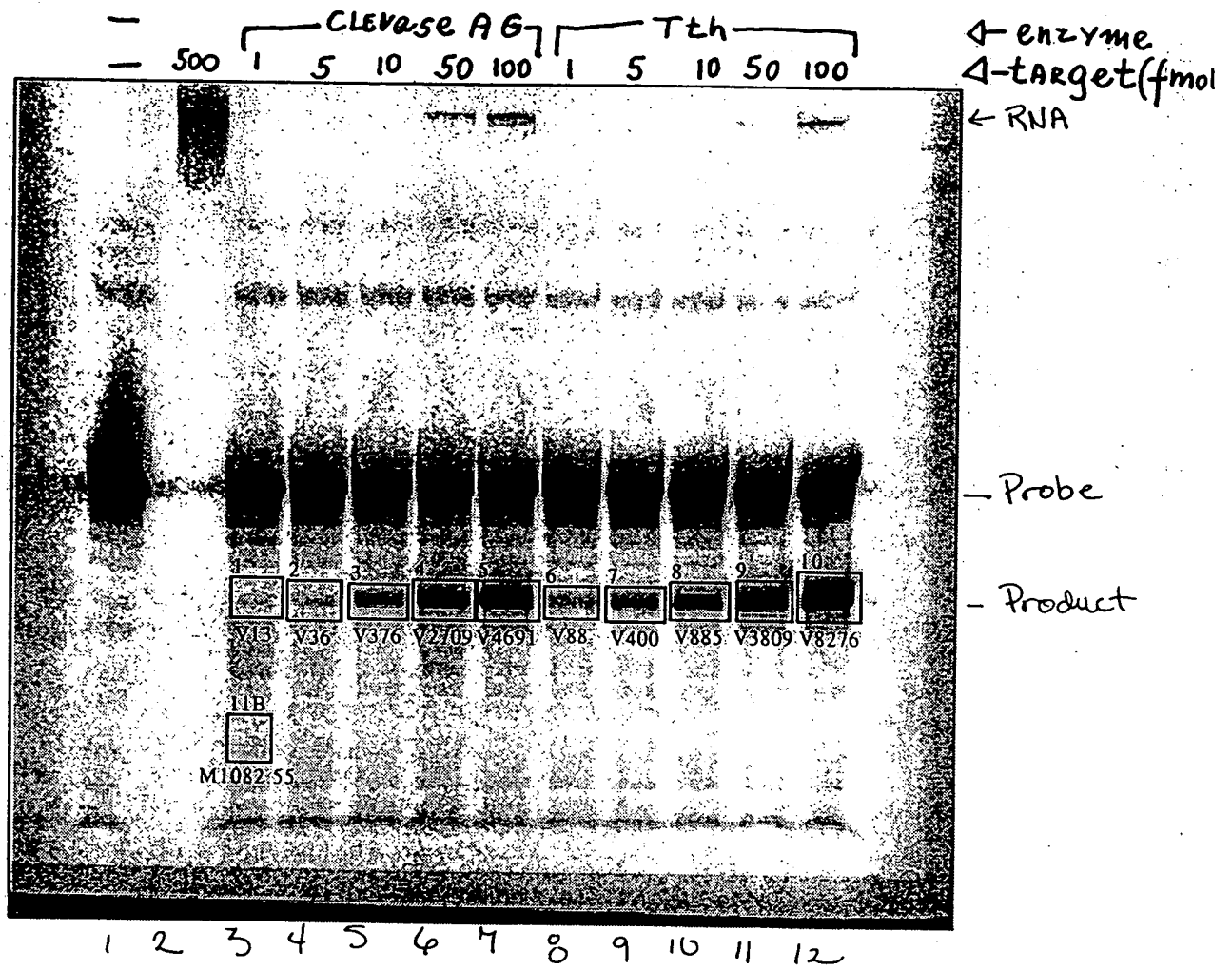
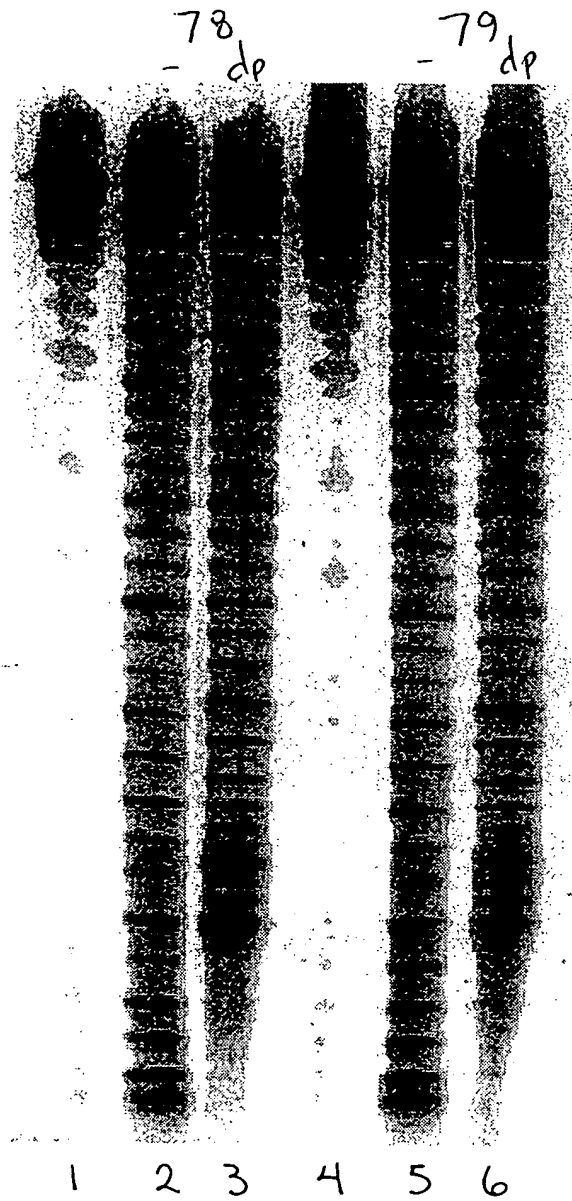


FIGURE 55



10074328.021202

FIGURE 56

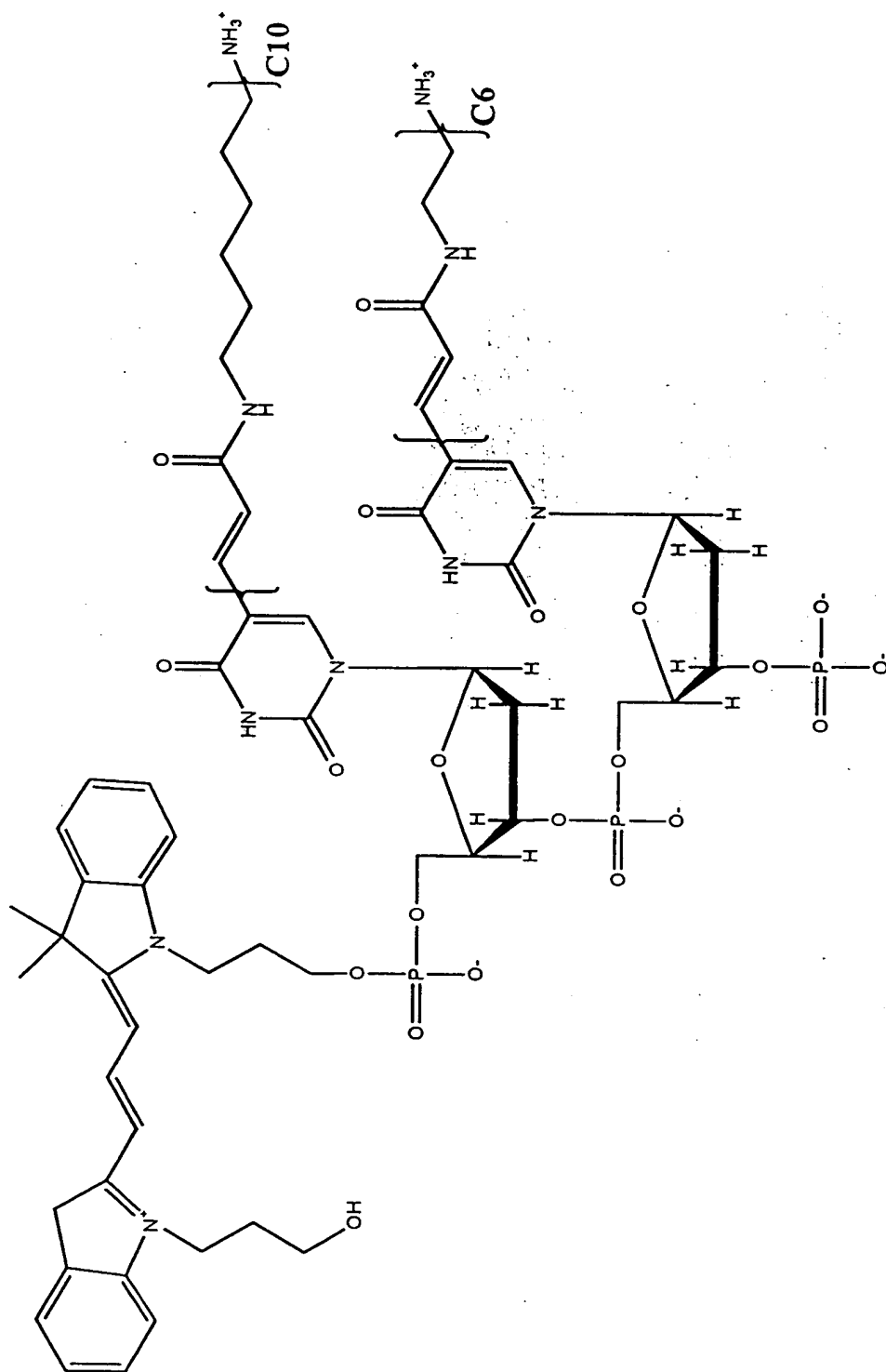
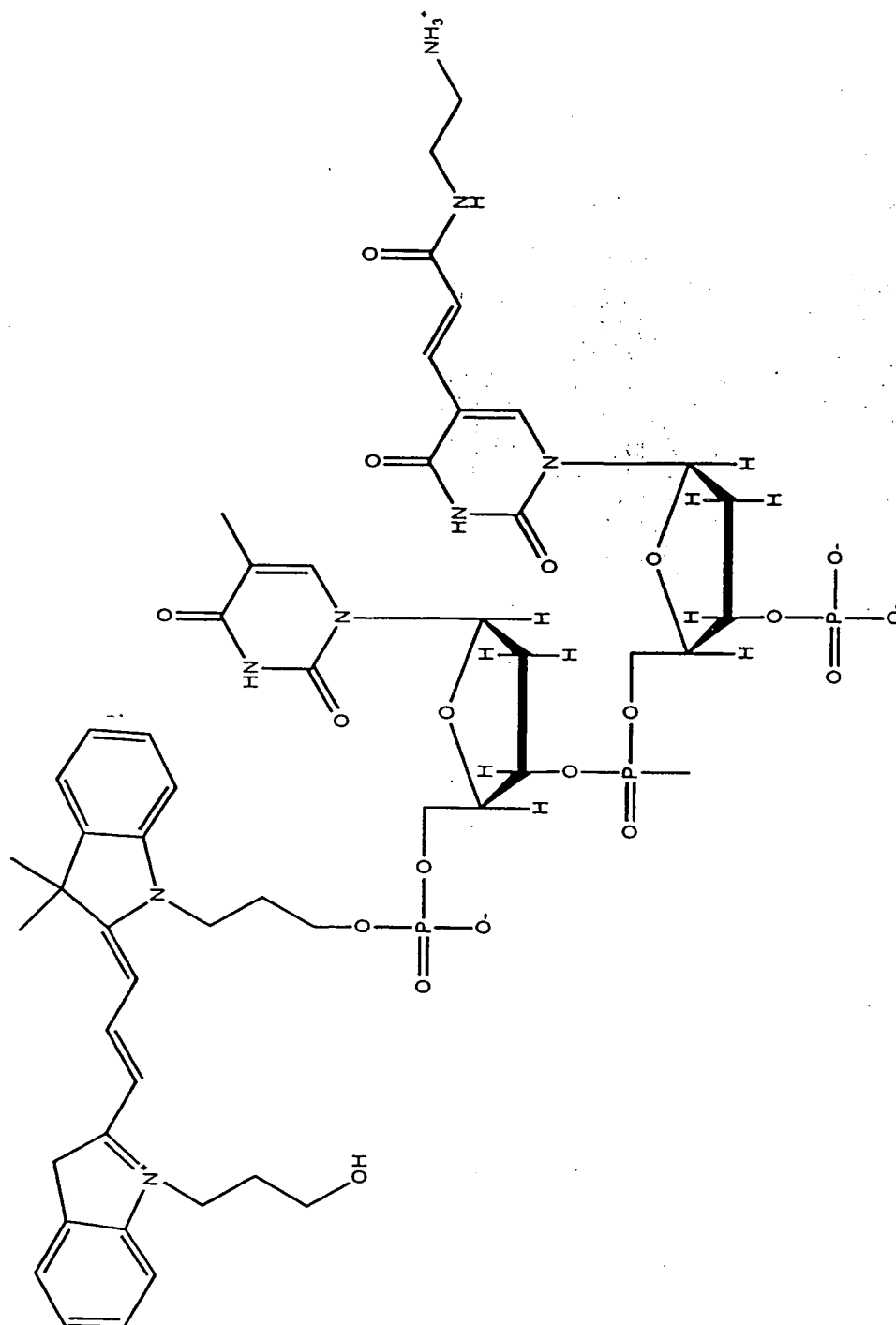
**70** (C10 aminoT's)**74** (C6 amino T's)

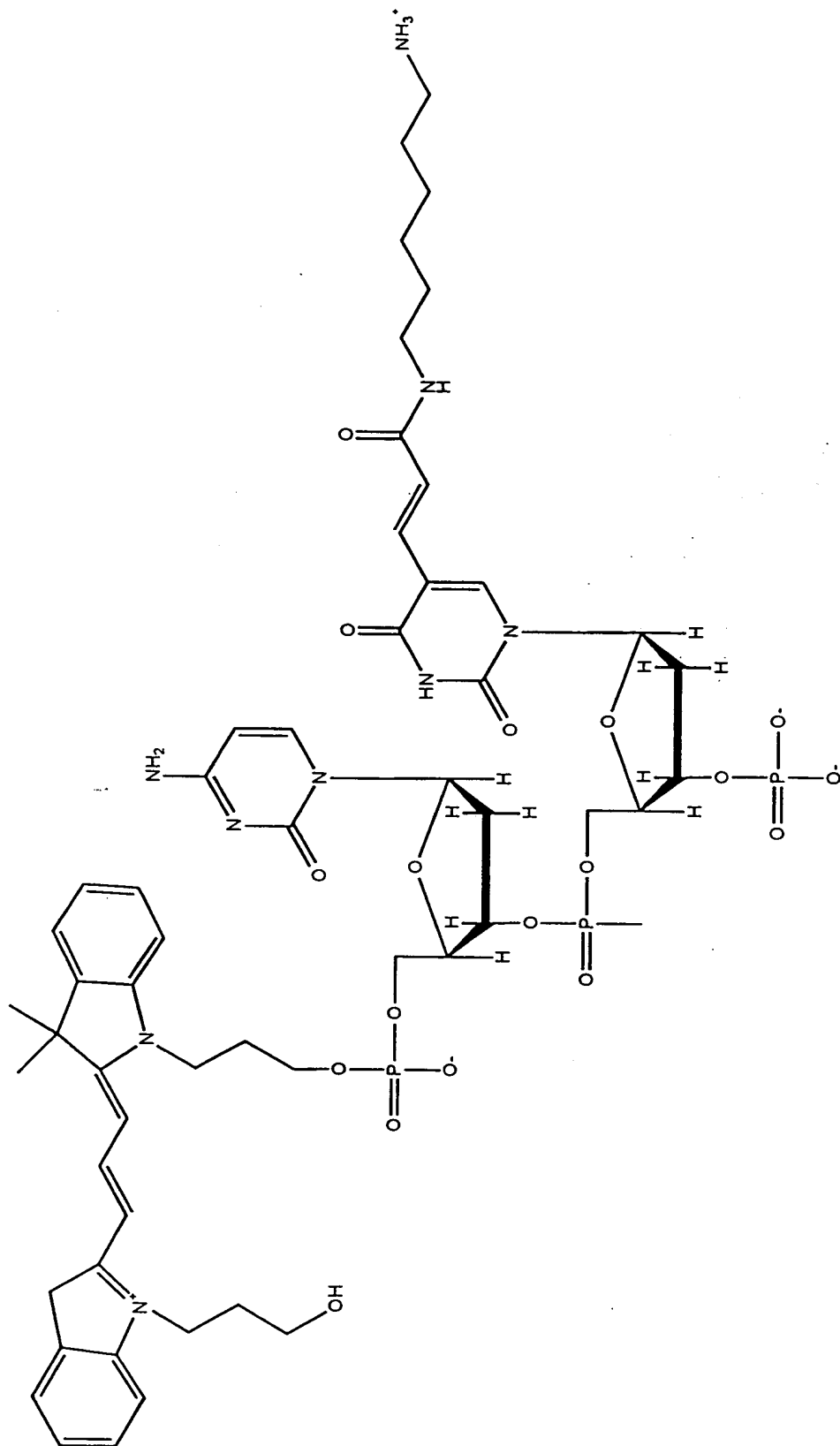
FIGURE 57 BEE42001

75



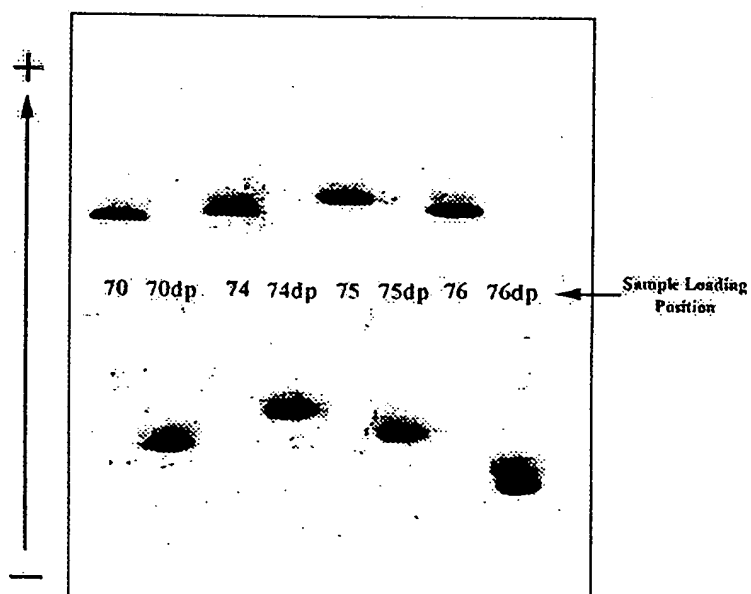
69

76




70

FIGURE 59



10074328.021202

[illegible]

A. 

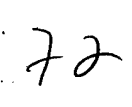
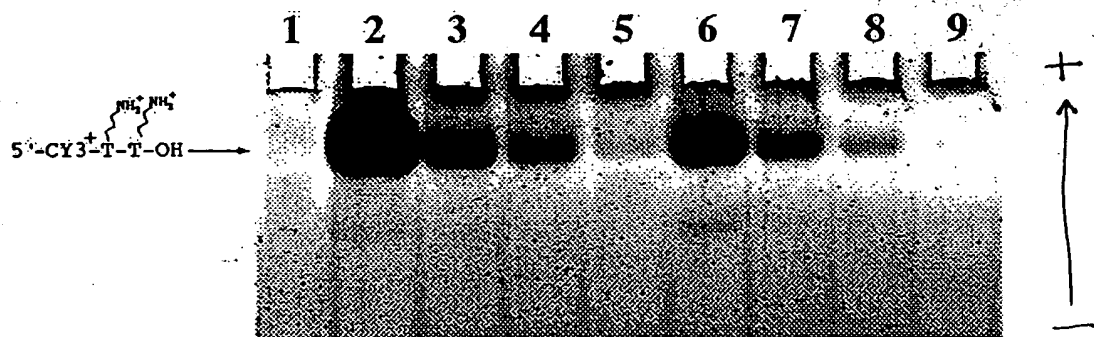




FIGURE 61



10074328.021202

202120" B2E4Z00T

FIGURE 62

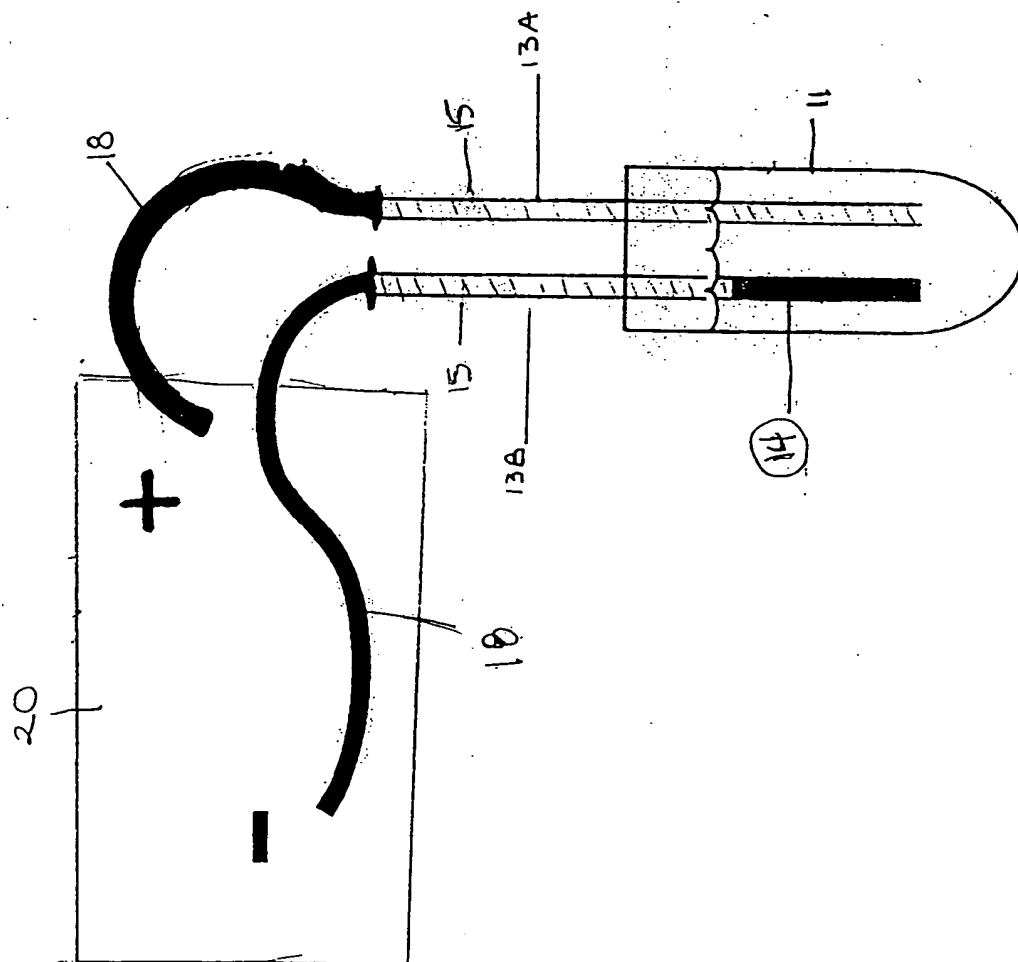
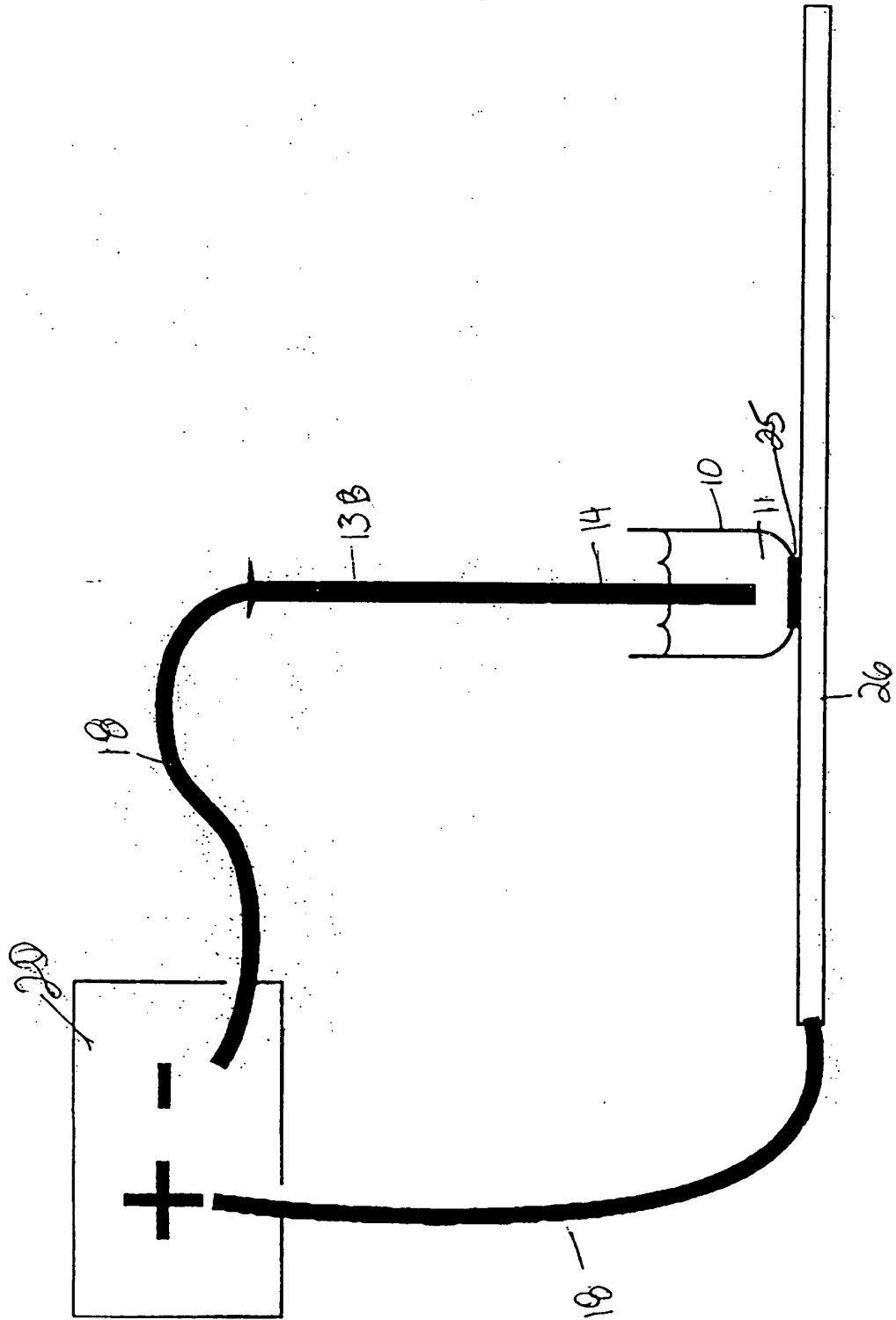


FIGURE 63



57

FIGURE 64

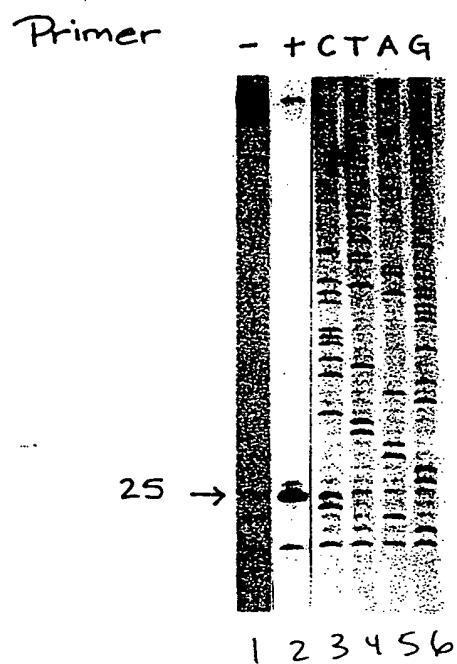
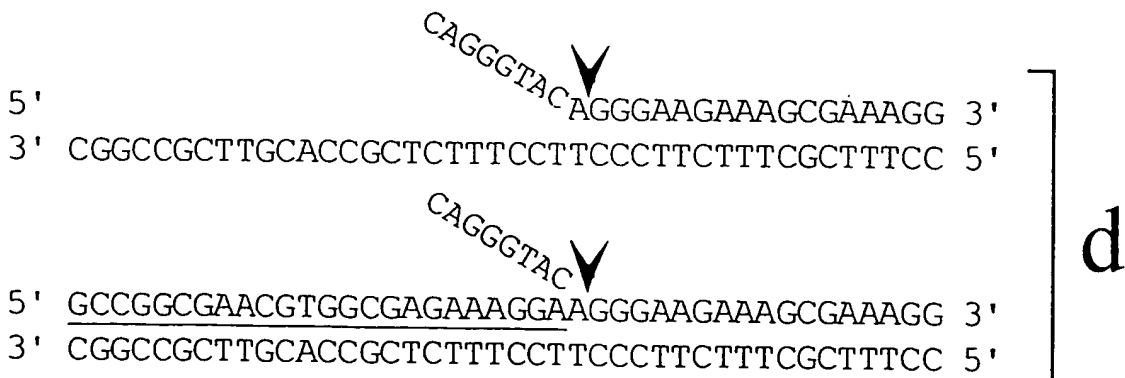
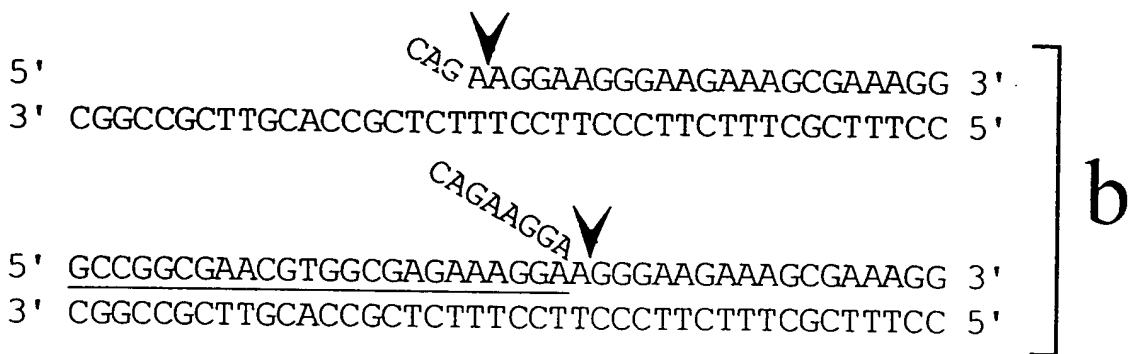
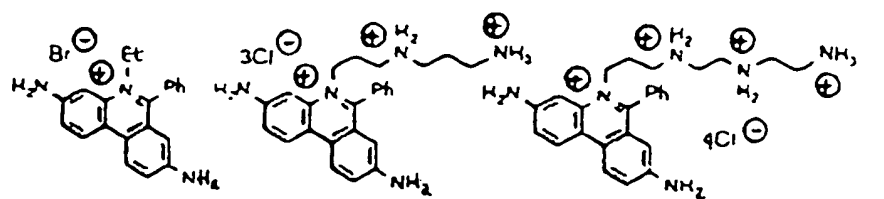


FIGURE 65

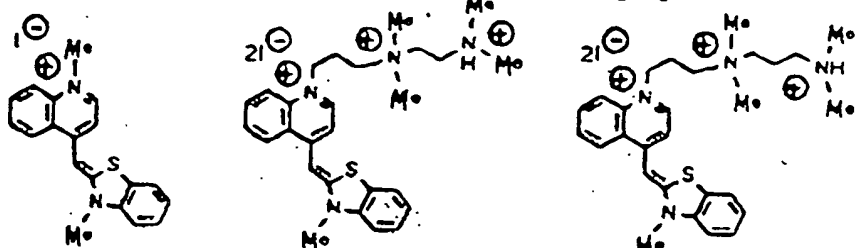


10074329.021202

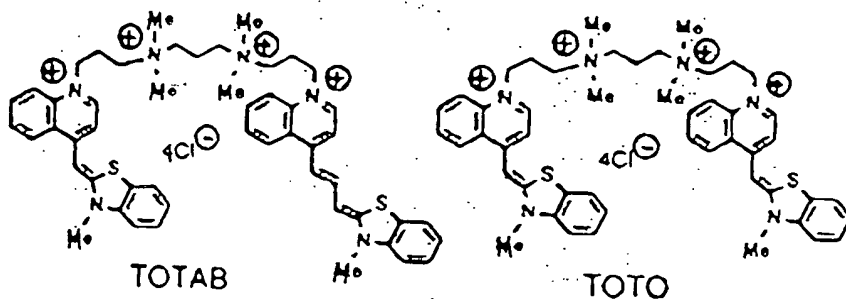
FIGURE 66



Ethidium Bromide (1,3-propanediamino)-propidium (diethylenetriamino)-propidium

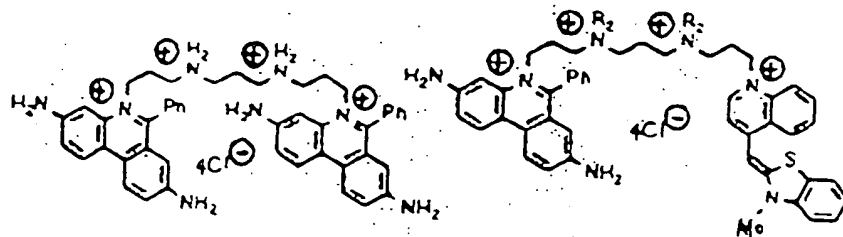


Thiazole Orange (N,N'-tetramethyl-1,2-ethanediamino)-propyl thiazole orange (N,N'-tetramethyl-1,3-propanediamino)-propyl thiazole orange



TOTAB

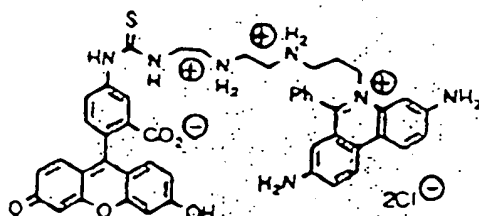
TOTO



EtbD

TOED1  
TOED2

(R = H)  
(R = CH<sub>3</sub>)



FED

10074328.021202

78